

## **Supplemental Information to:**

# **Microbial domestication signatures of *Lactococcus lactis* can be reproduced by experimental evolution**

Herwig Bachmann<sup>a,b,e</sup>, Marjo J.C. Starrenburg<sup>a,b</sup>, Douwe Molenaar<sup>a,b,e</sup>, Michiel  
Kleerebezem<sup>a,b,c,l</sup>, Johan E.T. van Hylckama Vlieg<sup>a,b,d</sup>

<sup>a</sup>NIZO food research, P.O. Box 20, 6710 BA Ede, The Netherlands; <sup>b</sup>Kluyver Centre for Genomics of  
Industrial Fermentation, Delft, The Netherlands; <sup>c</sup>Wageningen University, Laboratory for  
Microbiology, Dreijenplein 10, 6703HB Wageningen, The Netherlands; <sup>d</sup>Danone Research, R.D. 128,  
91767 Palaiseau Cedex, France; <sup>e</sup>Vrije Universiteit Amsterdam, Systems Bioinformatics IBIVU, De  
Boelelaan 1085, 1081HV Amsterdam, The Netherlands

## ***L. lactis* dairy strains**

*Lactococcus lactis* IL594 was isolated from a dairy starter culture and is the ancestor of the plasmid cured and fully sequenced strain IL1403 (Chopin *et al.* 1984; Bolotin *et al.* 2001). The plasmids of IL594 encode traits that are relevant for performance in the dairy niche, including lactose utilization and an extracellular protease. From a phylogenetic perspective, the dairy isolate IL1403 and its ancestor IL594 are closely related to KF147 (Rademaker *et al.* 2007), and thereby strain IL594 provides an appropriate dairy-reference for comparison with strain KF147.

Typically dairy isolates like the MG1363 ancestor NCDO712 (Gasson 1983), SK11 (de Vos *et al.* 1989; Makarova *et al.* 2006), WG2 (Kok *et al.* 1988), NCDO0762 (Kiwaki *et al.* 1989), FG2, HP, CJ, LW1413, 104, LW1484 (Christensson *et al.* 2001), LW1999, LW2000, LW2001, LW2003, LW2004, LW2005, LW2006, LW2015 (Ward *et al.* 2004), E8, AM1, AM2, KH (Exterkate *et al.* 1993; Rademaker *et al.* 2007) and AC1 (Bockelmann *et al.* 1989) harbor extracellular proteases that are described to be key enzymes for rapid growth in milk (Kunji *et al.* 1996). The importance of extracellular proteases for lactococcal growth in milk was one of the main reasons why we introduced a protease encoding plasmid into KF147 before we started the experimental evolution.

## ***Fitness assays***

The fitness of the adapted strains relative to the parental strain was determined in competition experiments after one- and three-days of incubation in milk. These two time-points represent the time required for well-adapted strains to reach their maximum cell density and the maximum time between serial transfers throughout the 1000-generation experimental evolution, respectively. After one day, the fitness of

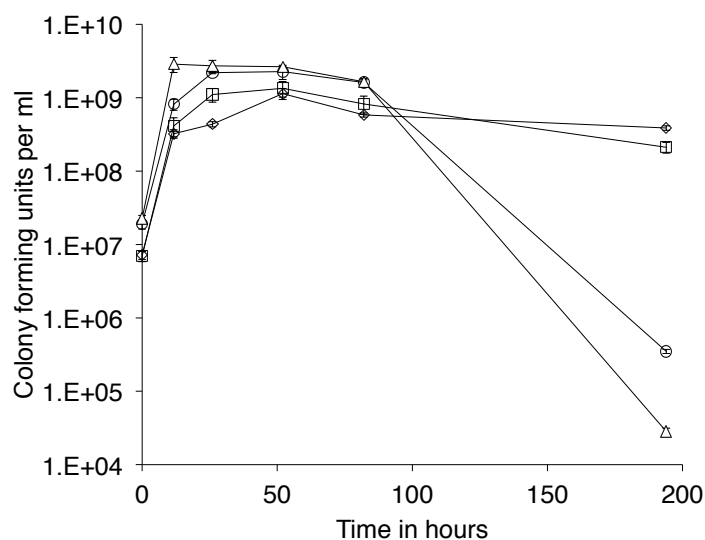
strains NZ5521, and NZ5523 was significantly higher than that of the parental strain KF147. With the extended incubation of three days, the relative fitness of all adapted strains (NZ5521, NZ5522, and NZ5523) was significantly higher than KF147 (Supplemental Figure 2).

### ***Transcriptome analysis of cells harvested in stationary phase***

Transcriptome analysis of cells from stationary phase resulted in 368 differentially expressed genes ( $p < 0.001$ ), (Supplemental Table 4). Similarities between the dairy isolate IL594 and strains NZ5521 and NZ5522 are recognized as expression levels close to the diagonal line in Supplemental Figure 8. In contrast, the expression levels of NZ5523 fall mainly on the horizontal line going through the origin of the graph in Supplemental Figure 8, indicating that these genes are expressed at a similar level to in the wild type KF147. We would like to note that due to the slow growth rate of KF147 and NZ5523 in milk it was difficult to accurately determine when cells reached the stationary phase. Transcriptome samples for all cultures were taken after 2 days of growth in milk. Figure 1c shows that at this stage cultures are not fully acidified but they have reached a pH that does not permit any further growth Supplemental Figure 7. For this reason some transcriptional changes like the ones related to a decrease in pH might not be caused by mutational changes in the adapted strain but rather by the time of sampling. Choosing a longer incubation period for strains KF147 and NZ5523 could have eliminated the difference in pH at the time of sampling, however these strains would have been in a non-growing stage for much longer than the comparison samples. Overall the stationary phase data supports the conclusion that NZ5521 and NZ5522 converge towards a dairy isolate at the transcriptional level.

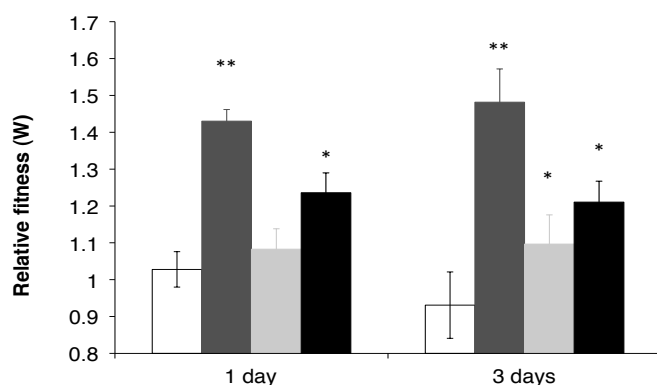
## ***Genome rearrangements***

The Illumina sequencing data was analyzed using the BRESEQ software package (Barrick et al. 2009), which allows the detection of new sequence junctions in the re-sequenced strains. This analysis did not result in conclusive evidence for genome rearrangements in any of the adapted strains.



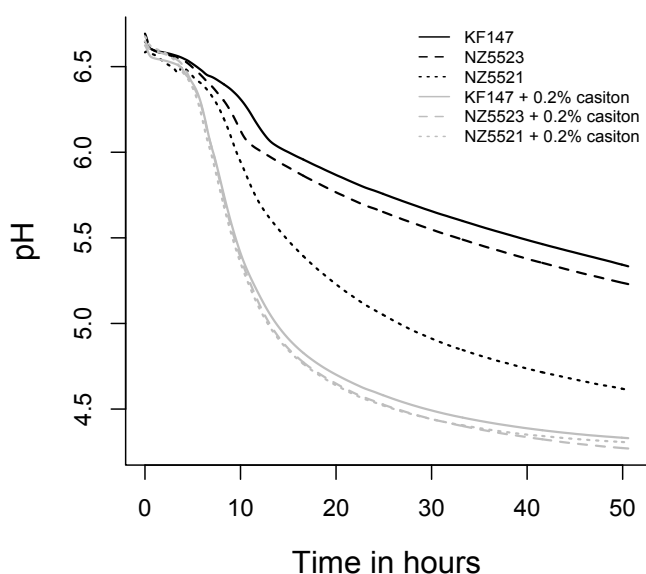
*Supplemental Figure 1*

Growth and viability of the adapted isolates in milk. The amount of colony forming units (y-axis) was determined for the wild type KF147 (◇) and the adapted isolates NZ5521 (△), NZ5522 (○) and NZ5523 (□) up to 194 hours of incubation in milk. The amount of colony forming units is clearly increased but the long-term survival seems much lower for strains NZ5521 and NZ5522 as compared to KF147 and NZ5523. The decreased survival is most likely caused by the lower pH of these cultures throughout stationary phase (see also Figure 1). Error bars represent standard deviation (n=4).



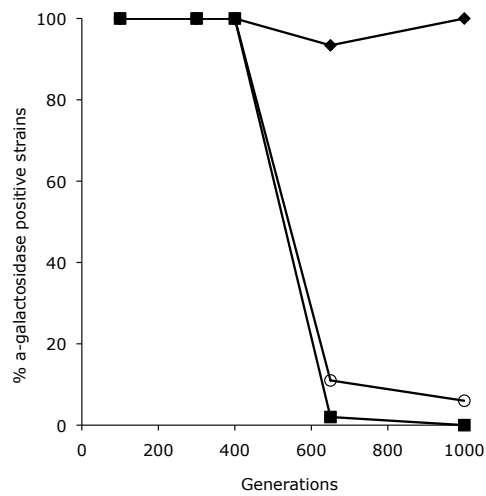
*Supplemental Figure 2*

Relative fitness of the wild type strain KF147 (white), NZ5521 (dark gray), NZ5522 (light gray) and NZ5523 (black) if grown in co-culture with strain KF147<sup>RIF</sup>. Relative fitness (W) (y-axis) was determined 1 and 3 days (x-axis) after inoculation of the co-cultures. Experimental evolution led to increased fitness of all adapted strains. Error bars show standard deviation (n=4). Significance was calculated using a two-tailed t-test comparing each sample of both time points to the wild type strain KF147; \* p < 0.05, \*\* p<0.01.



*Supplemental Figure 3*

Effect of casein hydrolysate on acidification profiles of KF147 and adapted strains. Acidification profiles in milk with and without the supplementation of 0.2% casein hydrolysate (Bacto tryptone or Casiton) (Becton Dickinson, Sparks, MD, USA). The curves show KF147 (solid lines), NZ5523 (dashed lines), NZ5521 (dotted lines). Strains were grown in milk (black lines) or in milk supplemented with 0.2% casein hydrolysate (gray lines). The supplementation of milk with casein hydrolysate is sufficient to overcome most growth limitations in milk and lead to similar acidification profiles of the adapted and the wild type KF147 strain.



*Supplemental Figure 4*

Fraction of  $\alpha$ -galactosidase positive strains during the experimental evolution experiment. Serial propagation cultures SP2 (■) and SP3 (○) revealed a decrease of  $\alpha$ -galactosidase-positive strains (y-axis) between 400 and 650 generations of adaptation. Serial propagation culture SP1 (◆) showed the appearance of the  $\alpha$ -galactosidase-negative subpopulation after 650 generations, which was subsequently replaced by  $\alpha$ -galactosidase-positive strains.

```

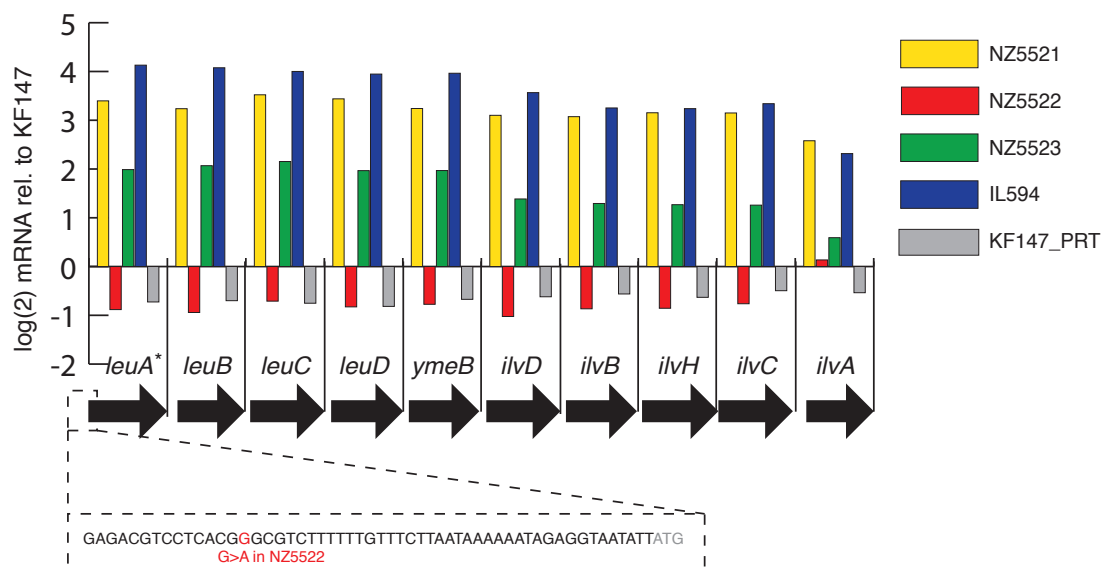
NZ5521_NZ5522_oppC      ATGACGAGAAAAAA-CACAAAAATTCCTTTCATTAGTTCACTCAATCAAGAACTAAAGAAATGATAAATTAGCAA*
KF147_oppC_incl_79_bp_us ATGACGAGAAAAAA-CACAAAAATTCCTTTCATTAGTTCACTCAATCAAGAACTAAAGAAATGATAAATTAGCAA
KF147_oppC_pseudo      -----A
MG1363_oppC            ATGACGAGAAAAAA-CACAAAAATTCCTTTCATTAGTTCACTCAATCAAGAACTAAAGAAATGATAAATTAGCGA
SK11_LACR_D18          ATGACGAGAAAAAA-CACAAAAATTCCTTTCATTAGTTCACTCAATCAAGAACTAAAGAAATGATAAATTAGCGA
IL1403_oppC            ATGACGAGAAAAAA-CACAAAAATTCCTTTCATTAGTTCACTCAATCAAGAACTAAAGAAATGATAAATTAGCGA
1.....10.....20.....30.....40.....50.....60.....70.....80

*****
NZ5521_NZ5522_oppC      TGATTTCAACATTTTTCCTAGTTGCTGCTTTTCTAATCGT 120
KF147_oppC_incl_79_bp_us TGATTTCAACATTTTTCCTAGTTGCTGCTTTTCTAATCGT 120
KF147_oppC_pseudo      TGATTTCAACATTTTTCCTAGTTGCTGCTTTTCTAATCGT 120
MG1363_oppC            TGATTTCAACATTTTTCCTAGTTGCTGCTTTTCTAATCGT 120
SK11_LACR_D18          TGATTTCAACATTTTTCCTAGTTGCTGCTTTTCTAATCGT 120
IL1403_oppC            TGATTTCAACATTTTTCCTAGTTGCTGCTTTTCTAATCGT 120
.....90.....100.....110.....120

```

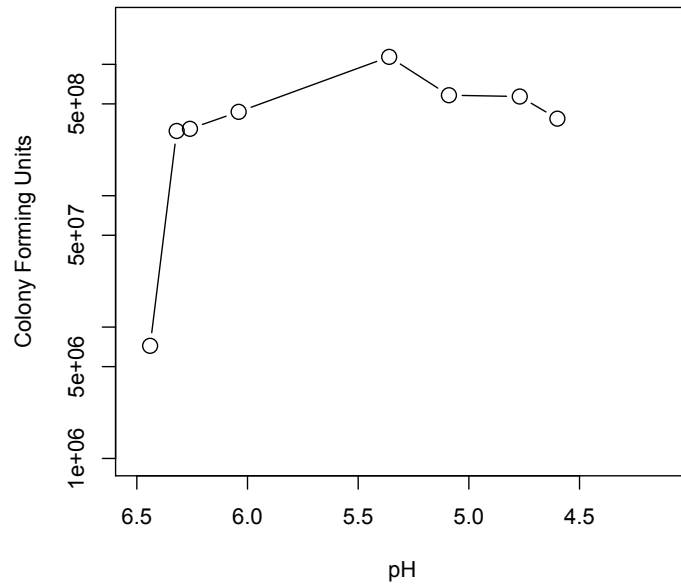
### Supplemental Figure 5

Alignment of *oppC* from of the adapted strains NZ5521 and NZ5522, the wild type gene including 79 bases of the upstream region and the wild type pseudo-gene (KF147\_oppC\_pseudo). The sequences are compared to the dairy strains MG1363 (NCBI Acc. Nr.: NC\_009004), IL1403 (NCBI Acc. Nr.: AE005176.1) and SK11(NCBI Acc. Nr.: NC\_008506.1). The deletion of an adenine residue at position 17 in NZ5521 and NZ5522 lead to an alternative start codon, which restores the full-length *oppC* gene as found in all sequenced dairy isolates.



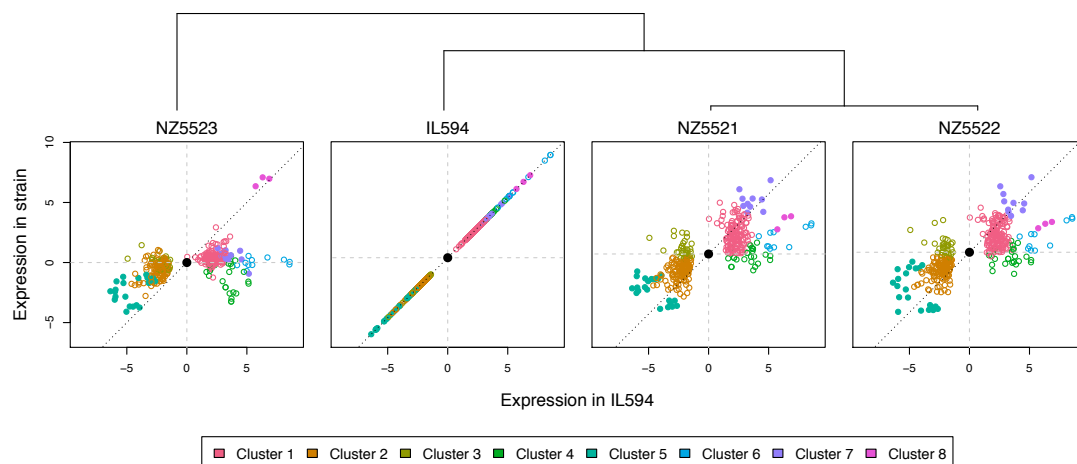
*Supplemental Figure 6*

Differential gene expression of a locus encoding genes involved in leucine, isoleucine and valine biosynthesis. During the logarithmic growth phase transcript levels of this locus were expressed at elevated levels in strains NZ5521, NZ5523 and IL594, while they were reduced in strain NZ5522 and KF147\_PRT. A mutation in the terminator/antiterminator promoter region was identified in strain NZ5522.



*Supplemental Figure 7*

Acidification and growth in milk. Colony forming units and pH were monitored throughout the growth of strain KF147 in milk. The maximum cell density was reached at approximately pH 5.5. Milk coagulates at approximately pH 5.1, which was taken as an indicator for a fully-grown culture throughout serial propagation.



*Supplemental Figure 8*

Genome-wide gene expression profiles of stationary cultures in milk. All strains are compared to with the wild type strain KF147. This plot was derived as described for Figure 2 and is based on the data given in Supplemental Table 4. Expression levels of genes falling either in the bottom left or the top right quadrant show transcript changes towards the levels found in IL594. Genes falling in the top left or bottom right quadrant show changes in the opposite direction compared to IL594. Expression levels of most significantly differential regulated genes of NZ5521 and NZ5522 fall close the diagonal line in the plot, indicating similarities with the dairy isolated IL594. Expression levels of NZ5523 fall mainly near the horizontal line going through the origin of the plot, indicating similar expression levels with KF147 and fewer changes toward strain IL594.

*Supplemental Table 1: Strains used in this study*

| Strain               | Description                                                                                      | Reference          |
|----------------------|--------------------------------------------------------------------------------------------------|--------------------|
| KF147                | <i>L. lactis</i> plant isolate with limited laboratory history                                   | Siezen et al. 2008 |
| KF147 pNZ521         | KF147 harbouring plasmid pNZ521                                                                  | this study         |
| KF147 <sup>rif</sup> | Spontaneous rifampicin resistant clone of KF147                                                  | this study         |
| NZ5521               | <i>L. lactis</i> KF147-1000 generations evolved in milk (single colony isolate from culture SP1) | this study         |
| NZ5522               | <i>L. lactis</i> KF147-1000 generations evolved in milk (single colony isolate from culture SP2) | this study         |
| NZ5523               | <i>L. lactis</i> KF147-1000 generations evolved in milk (single colony isolate from culture SP3) | this study         |
| IL594                | <i>L. lactis</i> IL594 - dairy isolate (parent strain of IL1403)                                 | Chopin et al. 1984 |

*Supplemental Table 2: Microarray hybridization scheme*

| Array Nr. | Dye       |                           |           |                           |
|-----------|-----------|---------------------------|-----------|---------------------------|
|           | Cy3       |                           | Cy5       |                           |
|           | Strain    | Growth phase <sup>1</sup> | Strain    | Growth phase <sup>1</sup> |
| 1         | NZ5521    | exp                       | NZ5521    | stat                      |
| 2         | NZ5521    | stat                      | KF147_PRT | stat                      |
| 3         | NZ5522    | exp                       | NZ5522    | stat                      |
| 4         | NZ5522    | stat                      | KF147_PRT | stat                      |
| 5         | NZ5523    | exp                       | KF147     | exp                       |
| 6         | NZ5523    | stat                      | NZ5523    | exp                       |
| 7         | IL594     | exp                       | IL594     | stat                      |
| 8         | IL594     | stat                      | KF147     | stat                      |
| 9         | KF147     | exp                       | IL594     | exp                       |
| 10        | KF147     | exp                       | KF147     | stat                      |
| 11        | KF147_PRT | exp                       | NZ5521    | exp                       |
| 12        | KF147_PRT | exp                       | NZ5522    | exp                       |
| 13        | KF147_PRT | exp                       | KF147     | exp                       |
| 14        | KF147_PRT | stat                      | KF147_PRT | exp                       |
| 15        | KF147     | stat                      | NZ5523    | stat                      |
| 16        | KF147     | stat                      | KF147_PRT | stat                      |

1) Cells were isolated either during exponential growth (exp) or in stationary phase (stat)

### Supplemental Table 3

Transcriptome data from logarithmically growing cells as compared to KF147. Selected genes show significant differential regulation ( $p < 0.001$ ) in at least one of the samples. This dataset was used for the generation of Figure 2. Columns with light grey headers show the  $\log(2)$  transformed regulation coefficient. Columns with dark grey headers show the corresponding p-value (*italics*). The cluster numbers correspond to the cluster numbers given in Figure 2.

| Feature ID | Gene          | Annotation                                                         | NZ5521_<br>log | NZ5522_<br>log | NZ5523_<br>log | IL594_<br>log | KF147prt_<br>log | NZ5521_<br>log | NZ5522_<br>log | NZ5523_<br>log | IL594_<br>log | KF147prt_<br>log | cluster |
|------------|---------------|--------------------------------------------------------------------|----------------|----------------|----------------|---------------|------------------|----------------|----------------|----------------|---------------|------------------|---------|
| LLKF_0150  | <i>ybfC</i>   | Hypothetical protein                                               | 0.379          | -0.133         | -0.122         | 2.480         | -0.008           | 0.512          | 0.843          | 0.880          | 0.000         | 0.987            | 1       |
| LLKF_0008  | <i>yabB</i>   | Transcriptional regulator, Cro/C1 family                           | 0.097          | -0.032         | -0.080         | 2.053         | -0.180           | 0.685          | 0.803          | 0.884          | 0.000         | 0.672            | 1       |
| LLKF_0028  | <i>yafE</i>   | Acetyltransferase, GNAT family                                     | -0.180         | 0.273          | 0.102          | 1.944         | 0.613            | 0.784          | 0.512          | 0.764          | 0.000         | 0.231            | 1       |
| LLKF_0054  | <i>yahB</i>   | Universal stress protein A                                         | -0.368         | 0.792          | 0.123          | 1.877         | -0.449           | 0.438          | 0.380          | 0.822          | 0.000         | 0.341            | 1       |
| LLKF_0061  | <i>cadA</i>   | Lead, cadmium, zinc, mercury transporting ATPase                   | -1.247         | -0.900         | -0.191         | 1.640         | 0.648            | 0.078          | 0.174          | 0.815          | 0.001         | 0.117            | 1       |
| LLKF_0081  | <i>acpD</i>   | Acyl carrier protein phosphodiesterase                             | 0.665          | -0.083         | -0.289         | 2.284         | -0.285           | 0.445          | 0.945          | 0.796          | 0.000         | 0.599            | 1       |
| LLKF_0127  | <i>ybeF-N</i> | Collagen adhesion protein, N-terminus (pseudogene)                 | 0.592          | 0.972          | 0.452          | 3.798         | 0.140            | 0.496          | 0.270          | 0.618          | 0.000         | 0.570            | 1       |
| LLKF_0128  | <i>ybeF-C</i> | Collagen adhesion protein, LPXTG-anchored, C-terminus (pseudogene) | 0.413          | 0.688          | 0.250          | 3.730         | 0.191            | 0.524          | 0.458          | 0.757          | 0.000         | 0.595            | 1       |
| LLKF_0146  | <i>ybfA</i>   | Hypothetical protein                                               | 0.542          | 0.480          | 0.440          | 2.028         | -0.309           | 0.446          | 0.493          | 0.525          | 0.000         | 0.494            | 1       |
| LLKF_0151  | <i>ybgA</i>   | Hypothetical protein                                               | -0.278         | -0.734         | -0.139         | 2.553         | -0.356           | 0.759          | 0.368          | 0.817          | 0.000         | 0.465            | 1       |
| LLKF_0225  | <i>ycdA</i>   | Hypothetical protein                                               | 0.220          | 0.346          | -0.096         | 2.956         | 0.714            | 0.803          | 0.687          | 0.934          | 0.000         | 0.141            | 1       |
| LLKF_0229  | <i>ycdE</i>   | Zinc-binding dehydrogenase                                         | 0.286          | 0.415          | -0.227         | 2.027         | 0.230            | 0.716          | 0.493          | 0.801          | 0.001         | 0.509            | 1       |
| LLKF_0238  | <i>yceA</i>   | Hypothetical protein                                               | 0.498          | 0.340          | 0.014          | 1.977         | 0.830            | 0.578          | 0.703          | 0.871          | 0.001         | 0.212            | 1       |
| LLKF_0239  | <i>yihA</i>   | Hypothetical protein, C-terminal fragment (pseudogene)             | 0.635          | -0.037         | 0.106          | 2.975         | 0.975            | 0.494          | 0.465          | 0.809          | 0.000         | 0.259            | 1       |
| LLKF_0240  | <i>yceD</i>   | Hypothetical protein                                               | 0.501          | 0.633          | 0.230          | 2.755         | 0.924            | 0.558          | 0.489          | 0.683          | 0.000         | 0.106            | 1       |
| LLKF_0347  | <i>ycjH</i>   | Hypothetical protein                                               | 0.588          | 0.737          | 0.025          | 2.861         | 0.353            | 0.395          | 0.291          | 0.903          | 0.000         | 0.405            | 1       |
| LLKF_0392  | <i>ahpC</i>   | Peroxiredoxin                                                      | 1.282          | 1.139          | -0.157         | 1.896         | 1.432            | 0.153          | 0.156          | 0.871          | 0.001         | 0.014            | 1       |
| LLKF_0398  | <i>optS</i>   | Oligopeptide ABC transporter, substrate-binding protein            | 0.409          | -1.297         | -0.037         | 3.477         | 0.482            | 0.598          | 0.084          | 0.977          | 0.000         | 0.282            | 1       |
| LLKF_0427  | <i>ldhB</i>   | L-lactate dehydrogenase                                            | 0.063          | -0.314         | 0.038          | 3.255         | -0.025           | 0.558          | 0.451          | 0.870          | 0.000         | 0.561            | 1       |
| LLKF_0445  | <i>groES</i>  | 10 kDa chaperonin GroES                                            | 0.764          | 1.385          | 0.008          | 2.218         | 1.639            | 0.342          | 0.130          | 0.921          | 0.000         | 0.008            | 1       |

| Feature ID | Gene             | Annotation                                               | NZ5521_<br>log | NZ5522_<br>log | NZ5523_<br>log | IL594_<br>og | KF147prt_<br>log | NZ5521_<br>log | NZ5522_<br>log | NZ5523_<br>log | IL594_<br>og | KF147prt_<br>log | cluster |
|------------|------------------|----------------------------------------------------------|----------------|----------------|----------------|--------------|------------------|----------------|----------------|----------------|--------------|------------------|---------|
| LLKF_0474  | <i>nifJ</i>      | Pyruvate dehydrogenase (ferredoxin/ferredoxin-dependent) | -1.400         | -0.924         | -0.168         | 1.945        | -0.059           | 0.105          | 0.256          | 0.800          | 0.000        | 0.639            | 1       |
| LLKF_0494  |                  | L-lactate/malate dehydrogenase                           | -0.348         | -0.517         | -0.268         | 1.456        | -0.528           | 0.573          | 0.392          | 0.700          | 0.001        | 0.148            | 1       |
| LLKF_0646  | <i>gltA</i>      | Citrate synthase                                         | 0.174          | -1.131         | -0.306         | 3.526        | 0.139            | 0.754          | 0.129          | 0.692          | 0.000        | 0.721            | 1       |
| LLKF_0647  | <i>citB</i>      | Aconitate hydratase                                      | -0.157         | -1.278         | -0.406         | 3.596        | -0.231           | 0.642          | 0.165          | 0.619          | 0.000        | 0.568            | 1       |
| LLKF_0648  | <i>icd</i>       | Isocitrate dehydrogenase [NADP]                          | -0.187         | -0.825         | -0.419         | 2.689        | -0.294           | 0.712          | 0.227          | 0.676          | 0.001        | 0.506            | 1       |
| LLKF_0731  | <i>yhcA</i>      | ABC transporter, ATP-binding and permease protein        | 0.487          | 0.472          | 0.068          | 2.222        | 0.328            | 0.438          | 0.462          | 0.915          | 0.000        | 0.437            | 1       |
| LLKF_0761  | <i>yheG</i>      | FabD/lysophospholipase-like protein, patatin family      | 0.135          | -0.026         | 0.170          | 1.519        | 0.375            | 0.689          | 0.978          | 0.843          | 0.001        | 0.332            | 1       |
| LLKF_0782  | <i>lrgA</i>      | Murein hydrolase exporter                                | 1.583          | 0.791          | 0.364          | 0.907        | 2.175            | 0.031          | 0.237          | 0.621          | 0.016        | 0.001            | 1       |
| LLKF_0789  | <i>manA</i>      | Mannose-6-phosphate isomerase                            | 0.099          | 0.128          | -0.034         | -0.004       | 2.145            | 0.816          | 0.795          | 0.824          | 0.687        | 0.001            | 1       |
| LLKF_0801  | <i>cblB/cgIB</i> | Cystathionine beta-lyase / Cystathionine gamma-lyase     | 0.253          | -0.786         | -2.032         | 2.935        | -0.512           | 0.660          | 0.392          | 0.013          | 0.000        | 0.407            | 1       |
| LLKF_0802  | <i>cysK1</i>     | Cysteine synthase                                        | 0.840          | -0.287         | -1.741         | 2.868        | -0.120           | 0.372          | 0.788          | 0.036          | 0.000        | 0.854            | 1       |
| LLKF_0839  | <i>yidE</i>      | Hypothetical protein                                     | 0.620          | 0.889          | 0.284          | 1.698        | 0.670            | 0.398          | 0.222          | 0.716          | 0.001        | 0.218            | 1       |
| LLKF_0858  | <i>yigC</i>      | Arsenate reductase family protein                        | -0.006         | -0.466         | 0.094          | 2.889        | -0.266           | 0.986          | 0.509          | 0.921          | 0.000        | 0.534            | 1       |
| LLKF_0903  | <i>yjaE</i>      | ABC transporter, phage infection protein                 | 0.398          | 0.268          | 0.795          | 2.628        | 0.186            | 0.690          | 0.793          | 0.394          | 0.001        | 0.733            | 1       |
| LLKF_0916  | <i>yjbB</i>      | Hypothetical protein                                     | 0.001          | 0.364          | 0.138          | 1.652        | 0.298            | 0.841          | 0.577          | 0.858          | 0.000        | 0.438            | 1       |
| LLKF_0917  | <i>tcsK2</i>     | Two-component sensor protein kinase                      | -0.106         | 0.131          | 0.128          | 1.522        | 0.073            | 0.759          | 0.832          | 0.881          | 0.001        | 0.748            | 1       |
| LLKF_0918  | <i>tcsR2</i>     | Two-component response regulator                         | 0.135          | 0.365          | 0.177          | 1.571        | 0.511            | 0.753          | 0.576          | 0.811          | 0.001        | 0.194            | 1       |
| LLKF_0920  | <i>ppiB</i>      | Peptidyl-prolyl cis-trans isomerase                      | 0.064          | 0.338          | 0.140          | 1.481        | 0.281            | 0.836          | 0.590          | 0.866          | 0.001        | 0.469            | 1       |
| LLKF_0921  | <i>yjbE</i>      | General stress protein with S1-type RNA-binding domain   | 0.009          | 0.442          | 0.490          | 1.603        | 0.343            | 0.901          | 0.474          | 0.403          | 0.000        | 0.350            | 1       |
| LLKF_0922  | <i>yjbF</i>      | Hypothetical protein                                     | -0.171         | 0.273          | 0.191          | 1.397        | 0.613            | 0.799          | 0.680          | 0.798          | 0.001        | 0.107            | 1       |
| LLKF_0928  | <i>mleS</i>      | NAD-dependent malic enzyme                               | 0.463          | 0.146          | 0.073          | 2.470        | -0.247           | 0.532          | 0.778          | 0.833          | 0.000        | 0.600            | 1       |
| LLKF_0929  | <i>mleP</i>      | Malate/lactate antiporter                                | 0.490          | 0.546          | 0.389          | 3.394        | -0.113           | 0.514          | 0.470          | 0.614          | 0.000        | 0.623            | 1       |
| LLKF_0959  | <i>yjfG</i>      | Hypothetical protein                                     | 0.232          | 0.615          | 0.614          | 1.530        | 0.191            | 0.739          | 0.360          | 0.318          | 0.001        | 0.643            | 1       |
| LLKF_0981  | <i>hrcA</i>      | Heat-inducible transcription repressor HrcA              | 0.261          | 1.028          | 0.315          | 3.181        | 2.221            | 0.861          | 0.443          | 0.852          | 0.001        | 0.017            | 1       |
| LLKF_1089  | <i>rex</i>       | Redox-sensing transcriptional repressor                  | -0.792         | -0.315         | 0.402          | 1.741        | 1.653            | 0.220          | 0.644          | 0.547          | 0.000        | 0.002            | 1       |
| LLKF_1169  | <i>yjfl</i>      | Hypothetical protein                                     | 1.276          | 1.011          | 0.737          | 1.703        | 1.438            | 0.062          | 0.115          | 0.213          | 0.000        | 0.005            | 1       |
| LLKF_1208  | <i>als</i>       | Alpha-acetolactate synthase                              | 0.086          | 0.552          | -0.762         | 1.637        | -1.396           | 0.763          | 0.460          | 0.213          | 0.001        | 0.007            | 1       |
| LLKF_1271  | <i>aldB</i>      | Alpha-acetolactate decarboxylase                         | 2.295          | 0.620          | 0.238          | 1.958        | -0.482           | 0.008          | 0.400          | 0.777          | 0.000        | 0.277            | 1       |
| LLKF_1272  | <i>aldR</i>      | Translation initiation inhibitor                         | 2.310          | 0.449          | 0.620          | 2.136        | -0.497           | 0.005          | 0.505          | 0.318          | 0.000        | 0.236            | 1       |
| LLKF_1312  | <i>ymhA</i>      | Trans-acting positive regulator                          | 0.512          | 0.765          | 0.073          | 1.805        | -0.099           | 0.493          | 0.334          | 0.822          | 0.001        | 0.668            | 1       |
| LLKF_1331  | <i>ymjE</i>      | Glycosyltransferase, family 2                            | 0.169          | 0.871          | 0.814          | 1.776        | -0.068           | 0.759          | 0.165          | 0.166          | 0.000        | 0.715            | 1       |
| LLKF_1363  | <i>rdrB</i>      | Transcriptional regulator, DeoR family                   | 0.570          | 0.128          | -0.119         | 2.263        | 0.581            | 0.558          | 0.786          | 0.910          | 0.001        | 0.105            | 1       |
| LLKF_1389  | <i>yneB</i>      | Esterase/lipase                                          | 1.083          | 0.345          | 0.014          | 2.147        | 0.076            | 0.133          | 0.646          | 0.992          | 0.000        | 0.877            | 1       |
| LLKF_1390  | <i>yneC</i>      | Hypothetical protein                                     | 0.791          | 0.156          | -0.194         | 3.495        | 0.784            | 0.257          | 0.850          | 0.836          | 0.000        | 0.074            | 1       |
| LLKF_1392  | <i>arsD</i>      | Arsenical resistance operon trans-acting repressor       | 0.093          | -0.128         | -0.161         | 2.850        | -0.141           | 0.776          | 0.838          | 0.865          | 0.000        | 0.681            | 1       |
| LLKF_1393  | <i>arsC</i>      | Arsenate reductase                                       | 0.476          | 0.192          | 0.101          | 3.266        | 0.073            | 0.537          | 0.803          | 0.919          | 0.000        | 0.810            | 1       |

| Feature ID | Gene          | Annotation                                                                            | NZ5521_<br>log | NZ5522_<br>log | NZ5523_<br>log | IL594_<br>og | KF147prt_<br>log | NZ5521_<br>log | NZ5522_<br>log | NZ5523_<br>log | IL594_<br>og | KF147prt_<br>log | cluster |
|------------|---------------|---------------------------------------------------------------------------------------|----------------|----------------|----------------|--------------|------------------|----------------|----------------|----------------|--------------|------------------|---------|
| LLKF_1422  | <i>ldhL</i>   | L-lactate dehydrogenase                                                               | 0.272          | 0.262          | 0.098          | 3.708        | 1.126            | 0.650          | 0.622          | 0.902          | 0.000        | 0.020            | 1       |
| LLKF_1423  | <i>pyk</i>    | Pyruvate kinase                                                                       | 1.287          | 1.524          | 0.429          | 1.895        | 1.130            | 0.063          | 0.027          | 0.543          | 0.000        | 0.018            | 1       |
| LLKF_1424  | <i>pfkA</i>   | 6-phosphofructokinase                                                                 | 1.127          | 1.816          | 0.450          | 2.164        | 1.104            | 0.109          | 0.014          | 0.487          | 0.000        | 0.022            | 1       |
| LLKF_1427  | <i>ynhC</i>   | Toxic anion resistance protein                                                        | 0.147          | 0.358          | -0.016         | 1.579        | -0.396           | 0.753          | 0.589          | 0.891          | 0.001        | 0.407            | 1       |
| LLKF_1557  | <i>yohD</i>   | Hypothetical protein                                                                  | 0.614          | 0.723          | -0.022         | 2.523        | -0.559           | 0.433          | 0.357          | 0.934          | 0.000        | 0.239            | 1       |
| LLKF_1583  | <i>ypaI</i>   | Short-chain alcohol dehydrogenase                                                     | 0.848          | 0.766          | 0.411          | 1.825        | 0.113            | 0.171          | 0.208          | 0.511          | 0.000        | 0.780            | 1       |
| LLKF_1664  | <i>ypiE-N</i> | Hypothetical protein , N-terminal fragment (pseudogene)                               | -0.595         | -0.447         | 0.295          | 2.841        | -0.329           | 0.496          | 0.626          | 0.789          | 0.000        | 0.538            | 1       |
| LLKF_1667  | <i>ypiJ-C</i> | Hypothetical protein , C-terminal fragment (pseudogene)                               | 0.793          | 0.218          | -0.170         | 2.300        | -0.386           | 0.345          | 0.824          | 0.887          | 0.000        | 0.450            | 1       |
| LLKF_1668  | <i>ypiJ-N</i> | Hypothetical protein , N-terminal fragment (pseudogene)                               | 0.545          | 0.582          | 0.194          | 3.357        | 1.198            | 0.571          | 0.593          | 0.823          | 0.000        | 0.094            | 1       |
| LLKF_1669  | <i>ypiK</i>   | Hypothetical protein                                                                  | 0.624          | 0.076          | -0.218         | 3.738        | 0.600            | 0.537          | 0.957          | 0.875          | 0.000        | 0.313            | 1       |
| LLKF_1742  | <i>amtB</i>   | Ammonium/methylammonium transporter                                                   | 0.833          | -0.039         | 0.266          | 2.660        | 0.739            | 0.301          | 0.974          | 0.800          | 0.000        | 0.136            | 1       |
| LLKF_1778  | <i>yqgF</i>   | Hypothetical protein                                                                  | -0.216         | 0.073          | -0.065         | 1.944        | 0.122            | 0.768          | 0.873          | 0.947          | 0.000        | 0.788            | 1       |
| LLKF_1779  | <i>tkl</i>    | Transketolase                                                                         | -0.161         | 0.143          | 0.168          | 1.900        | 0.080            | 0.803          | 0.747          | 0.812          | 0.000        | 0.588            | 1       |
| LLKF_1846  | <i>yreD</i>   | Hypothetical protein                                                                  | 0.918          | 0.824          | 0.029          | 3.721        | 0.014            | 0.226          | 0.269          | 0.781          | 0.000        | 0.760            | 1       |
| LLKF_1898  | <i>pepF</i>   | Oligoendopeptidase F                                                                  | -0.341         | -0.355         | 0.057          | 3.363        | -0.795           | 0.703          | 0.697          | 0.966          | 0.000        | 0.122            | 1       |
| LLKF_1925  | <i>ysbA</i>   | Hydrolase, HAD superfamily                                                            | 0.762          | 0.801          | 0.277          | 2.151        | 0.421            | 0.279          | 0.260          | 0.730          | 0.000        | 0.331            | 1       |
| LLKF_1927  | <i>ysbC</i>   | Hypothetical protein                                                                  | 1.031          | 0.599          | 0.277          | 2.040        | 0.379            | 0.188          | 0.493          | 0.756          | 0.001        | 0.500            | 1       |
| LLKF_1974  | <i>codY</i>   | Transcription pleiotropic repressor codY                                              | -0.392         | -0.355         | -0.091         | 3.421        | 0.186            | 0.657          | 0.733          | 0.781          | 0.000        | 0.575            | 1       |
| LLKF_1975  | <i>ysgA</i>   | Transcriptional regulator                                                             | -0.011         | 0.009          | 0.124          | 3.299        | 0.113            | 0.923          | 0.957          | 0.869          | 0.000        | 0.789            | 1       |
| LLKF_1976  | <i>pepO</i>   | Oligoendopeptidase O                                                                  | 0.252          | 0.127          | 0.070          | 3.524        | -0.788           | 0.724          | 0.853          | 0.899          | 0.000        | 0.089            | 1       |
| LLKF_1993  | <i>pp304</i>  | Phage protein                                                                         | 0.006          | 0.111          | -0.420         | 2.619        | -0.284           | 0.821          | 0.886          | 0.594          | 0.000        | 0.481            | 1       |
| LLKF_2051  | <i>uspA3</i>  | Universal stress protein A                                                            | 0.509          | 0.501          | -0.013         | 3.080        | 0.632            | 0.565          | 0.552          | 0.814          | 0.000        | 0.201            | 1       |
| LLKF_2056  | <i>ileS</i>   | Isoleucyl-tRNA synthetase                                                             | 0.578          | 0.213          | -0.013         | 2.275        | 1.007            | 0.453          | 0.679          | 0.931          | 0.000        | 0.127            | 1       |
| LLKF_2069  | <i>rlrB</i>   | Transcriptional regulator, LysR family                                                | 0.741          | 0.552          | -0.074         | 1.699        | 0.414            | 0.253          | 0.360          | 0.934          | 0.000        | 0.297            | 1       |
| LLKF_2085  | <i>ytgB</i>   | Hypothetical protein                                                                  | 1.149          | 2.657          | 0.859          | 2.303        | 1.079            | 0.233          | 0.010          | 0.341          | 0.001        | 0.072            | 1       |
| LLKF_2089  | <i>ytgD</i>   | Hypothetical protein                                                                  | 0.035          | 0.600          | 0.142          | 1.497        | 0.189            | 0.961          | 0.298          | 0.859          | 0.000        | 0.599            | 1       |
| LLKF_2098  | <i>ythA</i>   | Stress-responsive transcriptional regulator, PspC family                              | -0.794         | -0.250         | -0.832         | 2.689        | -0.963           | 0.218          | 0.720          | 0.144          | 0.000        | 0.037            | 1       |
| LLKF_2099  | <i>ythB</i>   | Stress-responsive transcriptional regulator, PspC family                              | -0.364         | 0.132          | -0.510         | 2.868        | -0.203           | 0.636          | 0.849          | 0.496          | 0.000        | 0.653            | 1       |
| LLKF_2100  | <i>ythC</i>   | Hypothetical protein                                                                  | -0.351         | 0.150          | -0.436         | 3.140        | -0.117           | 0.597          | 0.837          | 0.549          | 0.000        | 0.592            | 1       |
| LLKF_2101  | <i>acmB</i>   | N-acetylmuramoyl-L-alanine amidase                                                    | -0.048         | 0.662          | 0.196          | 1.908        | -0.265           | 0.958          | 0.371          | 0.846          | 0.000        | 0.558            | 1       |
| LLKF_2295  | <i>pepX</i>   | Xaa-Pro dipeptidyl-peptidase                                                          | 0.327          | 0.478          | -0.097         | 2.131        | -0.348           | 0.678          | 0.579          | 0.864          | 0.001        | 0.485            | 1       |
| LLKF_2296  | <i>yvdE</i>   | Glutamine amidotransferase, class I                                                   | 0.040          | 0.105          | -0.095         | 2.034        | -0.404           | 0.771          | 0.667          | 0.927          | 0.000        | 0.374            | 1       |
| LLKF_2389  | <i>ywbA</i>   | Methyltransferase                                                                     | -0.016         | 0.021          | -0.347         | 1.881        | 0.311            | 0.819          | 0.854          | 0.609          | 0.000        | 0.502            | 1       |
| LLKF_2398  | <i>adhE</i>   | Bifunctional protein: Alcohol dehydrogenase/ Acetaldehyde dehydrogenase [acetylating] | -0.442         | -1.447         | 1.284          | 1.670        | 3.501            | 0.595          | 0.110          | 0.059          | 0.031        | 0.000            | 1       |

| Feature ID | Gene        | Annotation                                                         | NZ5521_<br>log | NZ5522_<br>log | NZ5523_<br>log | IL594_<br>og | KF147prt_<br>log | NZ5521_<br>log | NZ5522_<br>log | NZ5523_<br>log | IL594_<br>og | KF147prt_<br>log | cluster |
|------------|-------------|--------------------------------------------------------------------|----------------|----------------|----------------|--------------|------------------|----------------|----------------|----------------|--------------|------------------|---------|
| LLKF_2416  | <i>yweD</i> | Hypothetical protein                                               | 0.023          | -0.268         | 0.201          | 2.790        | -0.054           | 0.933          | 0.839          | 0.901          | 0.001        | 0.802            | 1       |
| LLKF_2474  | <i>ywiG</i> | ABC transporter, ATP-binding protein                               | 0.215          | 0.339          | 0.059          | 1.594        | 0.701            | 0.738          | 0.638          | 0.890          | 0.001        | 0.109            | 1       |
| LLKF_2481  | <i>ywjA</i> | Hypothetical protein                                               | 0.141          | 0.052          | -0.043         | 1.813        | 0.135            | 0.835          | 0.903          | 0.974          | 0.001        | 0.799            | 1       |
| LLKF_2491  | <i>dnaJ</i> | Chaperone protein DnaJ                                             | -0.595         | -0.105         | -0.253         | 2.683        | -0.176           | 0.481          | 0.904          | 0.766          | 0.000        | 0.656            | 1       |
| LLKF_2506  | <i>yxcB</i> | Transcriptional regulator, TetR family                             | -0.294         | -0.455         | 0.347          | 1.673        | 0.688            | 0.678          | 0.514          | 0.620          | 0.000        | 0.109            | 1       |
| LLKF_0039  | <i>lplL</i> | Lipoate-protein ligase                                             | -0.615         | 0.020          | -0.219         | -3.514       | 0.663            | 0.420          | 0.856          | 0.816          | 0.000        | 0.164            | 2       |
| LLKF_0116  | <i>ybdE</i> | Aldo/keto reductase                                                | -1.347         | -0.892         | -0.400         | -2.182       | -0.062           | 0.099          | 0.290          | 0.600          | 0.000        | 0.721            | 2       |
| LLKF_0164  | <i>ybhC</i> | Hypothetical protein                                               | -1.546         | -1.581         | -0.226         | -2.382       | -0.625           | 0.058          | 0.046          | 0.825          | 0.000        | 0.182            | 2       |
| LLKF_0185  | <i>ybjJ</i> | Dihydroxyacetone kinase family protein                             | -0.303         | 0.508          | -0.317         | -2.044       | 0.030            | 0.683          | 0.526          | 0.686          | 0.001        | 0.540            | 2       |
| LLKF_0187  | <i>rpmB</i> | LSU ribosomal protein L28P                                         | -0.146         | 0.084          | -0.775         | -2.032       | 0.614            | 0.863          | 0.801          | 0.293          | 0.000        | 0.257            | 2       |
| LLKF_0253  | <i>fbp1</i> | Fructose-1,6-bisphosphatase                                        | -1.215         | -1.330         | -0.727         | -3.270       | -0.516           | 0.123          | 0.087          | 0.312          | 0.000        | 0.261            | 2       |
| LLKF_0256  | <i>ycfH</i> | Hypothetical protein                                               | -0.177         | 0.079          | -0.240         | -1.692       | -0.463           | 0.711          | 0.924          | 0.719          | 0.000        | 0.274            | 2       |
| LLKF_0269  | <i>acmA</i> | N-acetylmuramidase                                                 | -0.379         | -1.013         | 0.208          | -2.126       | -0.494           | 0.563          | 0.117          | 0.748          | 0.000        | 0.209            | 2       |
| LLKF_0270  | <i>nrdD</i> | Anaerobic ribonucleoside-triphosphate reductase                    | 0.488          | 0.061          | 0.154          | -1.947       | 0.706            | 0.384          | 0.936          | 0.841          | 0.000        | 0.051            | 2       |
| LLKF_0271  | <i>nrdG</i> | Anaerobic ribonucleoside-triphosphate reductase activating protein | 0.738          | 0.637          | 0.280          | -2.391       | -0.039           | 0.326          | 0.379          | 0.752          | 0.000        | 0.756            | 2       |
| LLKF_0334  | <i>rpsD</i> | SSU ribosomal protein S4P                                          | 0.737          | 0.205          | 0.034          | -2.093       | 0.716            | 0.258          | 0.774          | 0.954          | 0.000        | 0.077            | 2       |
| LLKF_0348  | <i>phnD</i> | Phosphonates ABC transporter, phosphonates-binding protein PhnD    | 1.023          | 0.090          | 0.957          | -2.313       | 0.686            | 0.234          | 0.706          | 0.161          | 0.000        | 0.190            | 2       |
| LLKF_0355  | <i>napC</i> | Multidrug-efflux transporter, MF superfamily                       | -0.593         | 0.670          | -1.353         | -3.314       | 0.549            | 0.505          | 0.430          | 0.061          | 0.000        | 0.332            | 2       |
| LLKF_0400  | <i>optB</i> | Oligopeptide ABC transporter, permease protein                     | 1.506          | -0.201         | 0.605          | -2.260       | 1.178            | 0.042          | 0.799          | 0.356          | 0.000        | 0.016            | 2       |
| LLKF_0401  | <i>optC</i> | Oligopeptide ABC transporter, permease protein                     | 0.728          | -0.550         | 0.528          | -1.904       | 0.150            | 0.305          | 0.475          | 0.442          | 0.000        | 0.740            | 2       |
| LLKF_0402  | <i>optD</i> | Oligopeptide ABC transporter, ATP-binding protein                  | 0.863          | -0.684         | 0.311          | -2.358       | -0.108           | 0.292          | 0.328          | 0.648          | 0.000        | 0.800            | 2       |
| LLKF_0403  | <i>optF</i> | Oligopeptide ABC transporter, ATP-binding protein                  | 1.211          | -0.616         | 0.444          | -2.280       | -0.080           | 0.120          | 0.426          | 0.588          | 0.000        | 0.625            | 2       |
| LLKF_0436  | <i>tyrS</i> | Tyrosyl-tRNA synthetase                                            | 0.124          | 0.899          | 0.161          | -1.886       | 0.012            | 0.545          | 0.238          | 0.871          | 0.000        | 0.805            | 2       |
| LLKF_0443  | <i>noxE</i> | NADH oxidase, H <sub>2</sub> O-forming                             | -0.096         | 1.344          | 1.195          | -1.600       | -0.120           | 0.894          | 0.036          | 0.028          | 0.000        | 0.766            | 2       |
| LLKF_0447  | <i>yeaA</i> | Zn-dependent hydrolase, beta-lactamase superfamily                 | -0.216         | -0.095         | -0.257         | -1.397       | -0.132           | 0.724          | 0.894          | 0.702          | 0.001        | 0.723            | 2       |
| LLKF_0468  | <i>ptcC</i> | PTS system, cellobiose-specific IIC component                      | -1.229         | -1.410         | 0.133          | -1.815       | 0.045            | 0.093          | 0.066          | 0.861          | 0.001        | 0.783            | 2       |
| LLKF_0479  | <i>yedE</i> | PTS system, beta-glucoside-specific IIA component                  | -1.543         | -1.082         | 0.444          | -2.373       | 0.633            | 0.063          | 0.169          | 0.544          | 0.000        | 0.151            | 2       |
| LLKF_0480  | <i>yedF</i> | PTS system, beta-glucoside-specific IIBC component                 | -0.756         | -1.124         | 1.040          | -2.299       | 0.715            | 0.303          | 0.113          | 0.090          | 0.000        | 0.182            | 2       |
| LLKF_0481  | <i>yeeA</i> | Glycosyl hydrolase, family 65                                      | -0.522         | -1.216         | 1.293          | -2.292       | 0.691            | 0.481          | 0.083          | 0.045          | 0.000        | 0.166            | 2       |
| LLKF_0482  | <i>pgmB</i> | Beta-phosphoglucomutase                                            | -0.442         | -1.082         | 1.206          | -2.387       | 0.453            | 0.588          | 0.162          | 0.080          | 0.000        | 0.331            | 2       |
| LLKF_0541  | <i>gltS</i> | Glutamate or arginine ABC transporter, substrate binding protein   | 0.817          | 0.947          | -0.276         | -2.920       | 1.174            | 0.463          | 0.395          | 0.856          | 0.000        | 0.101            | 2       |
| LLKF_0542  | <i>argE</i> | Acetylornithine deacetylase                                        | 0.367          | 0.513          | -0.259         | -2.694       | 1.094            | 0.521          | 0.643          | 0.830          | 0.000        | 0.101            | 2       |
| LLKF_0548  | <i>yfgG</i> | Membrane protein, OxaA/YidC family                                 | -0.519         | -0.827         | -0.243         | -1.591       | -0.153           | 0.454          | 0.204          | 0.739          | 0.001        | 0.499            | 2       |
| LLKF_0584  | <i>yfiC</i> | Acylphosphatase                                                    | -1.677         | -1.332         | -0.786         | -1.775       | -0.646           | 0.041          | 0.072          | 0.222          | 0.001        | 0.163            | 2       |
| LLKF_0640  | <i>pfl</i>  | Formate acetyltransferase                                          | -0.629         | -1.413         | -0.123         | -4.946       | -0.686           | 0.525          | 0.161          | 0.625          | 0.000        | 0.258            | 2       |
| LLKF_0655  | <i>ygiG</i> | Acetyltransferase, GNAT family                                     | -0.410         | -0.414         | -0.687         | -3.713       | -0.415           | 0.586          | 0.569          | 0.277          | 0.000        | 0.325            | 2       |

| Feature ID | Gene         | Annotation                                                                       | NZ5521_<br>log | NZ5522_<br>log | NZ5523_<br>log | IL594_<br>og | KF147prt_<br>log | NZ5521_<br>log | NZ5522_<br>log | NZ5523_<br>log | IL594_<br>og | KF147prt_<br>log | cluster |
|------------|--------------|----------------------------------------------------------------------------------|----------------|----------------|----------------|--------------|------------------|----------------|----------------|----------------|--------------|------------------|---------|
| LLKF_0656  | <i>ygiH</i>  | Hypothetical protein                                                             | -0.242         | -0.278         | -0.551         | -3.359       | -0.464           | 0.774          | 0.748          | 0.476          | 0.000        | 0.318            | 2       |
| LLKF_0849  | <i>trmU</i>  | tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase                     | -0.498         | 0.041          | -0.329         | -2.931       | -1.132           | 0.451          | 0.758          | 0.616          | 0.000        | 0.015            | 2       |
| LLKF_0894  | <i>rplS</i>  | LSU ribosomal protein L19P                                                       | -0.277         | -0.282         | -0.623         | -2.392       | -0.306           | 0.396          | 0.327          | 0.340          | 0.000        | 0.375            | 2       |
| LLKF_0914  | <i>yjaJ</i>  | Transcriptional regulator, LytR family                                           | -0.378         | -0.272         | -0.004         | -2.683       | -1.360           | 0.620          | 0.646          | 0.983          | 0.000        | 0.008            | 2       |
| LLKF_0935  | <i>yjdA</i>  | SAM-dependent methyltransferase                                                  | -1.349         | -0.605         | -0.504         | -1.326       | 0.014            | 0.028          | 0.282          | 0.342          | 0.001        | 0.975            | 2       |
| LLKF_0985  | <i>yjiB</i>  | N-acyl-L-amino acid amidohydrolase                                               | 0.029          | -0.077         | -0.177         | -4.913       | -1.419           | 0.975          | 0.912          | 0.846          | 0.000        | 0.008            | 2       |
| LLKF_1049  | <i>pp120</i> | Phage protein                                                                    | 0.109          | 0.329          | -0.135         | -1.711       | -0.966           | 0.900          | 0.682          | 0.900          | 0.001        | 0.044            | 2       |
| LLKF_1082  | <i>pp153</i> | Phage protein, tail component                                                    | 0.340          | 1.140          | -0.014         | -3.046       | -0.901           | 0.644          | 0.103          | 0.991          | 0.000        | 0.047            | 2       |
| LLKF_1083  | <i>pp154</i> | Phage protein, receptor-binding protein                                          | 0.456          | 1.206          | -0.183         | -2.895       | -0.883           | 0.567          | 0.109          | 0.861          | 0.000        | 0.164            | 2       |
| LLKF_1110  | <i>mntH1</i> | Manganese transport protein MntH, Nramp family                                   | 2.252          | 2.211          | 0.246          | -3.769       | 0.661            | 0.008          | 0.005          | 0.748          | 0.000        | 0.142            | 2       |
| LLKF_1131  | <i>ylbB</i>  | ABC transporter, permease protein                                                | -1.022         | -1.377         | 0.166          | -2.219       | -1.007           | 0.289          | 0.152          | 0.886          | 0.001        | 0.085            | 2       |
| LLKF_1149  | <i>yldC</i>  | Glyoxalase family protein                                                        | -1.294         | -1.321         | -0.768         | -1.735       | -1.032           | 0.077          | 0.055          | 0.217          | 0.000        | 0.026            | 2       |
| LLKF_1171  | <i>xpt</i>   | Xanthine phosphoribosyltransferase                                               | 0.736          | 0.388          | 0.048          | -3.762       | 0.101            | 0.268          | 0.535          | 0.915          | 0.000        | 0.721            | 2       |
| LLKF_1172  | <i>pbuX</i>  | Xanthine permease                                                                | 0.640          | 0.533          | 0.144          | -2.590       | 0.378            | 0.417          | 0.414          | 0.792          | 0.000        | 0.368            | 2       |
| LLKF_1243  | <i>ymcE</i>  | Transcriptional regulator, Xre family                                            | -0.281         | -0.511         | -0.003         | -2.553       | -1.247           | 0.682          | 0.449          | 0.914          | 0.000        | 0.014            | 2       |
| LLKF_1244  | <i>ymcF</i>  | Mucus-binding protein, N-terminal fragment (pseudogene)                          | -0.228         | -0.340         | 0.285          | -2.934       | -1.077           | 0.747          | 0.597          | 0.713          | 0.000        | 0.041            | 2       |
| LLKF_1317  | <i>lctO</i>  | L-lactate oxidase                                                                | -0.116         | 0.415          | 0.125          | -2.247       | 0.121            | 0.883          | 0.554          | 0.899          | 0.000        | 0.789            | 2       |
| LLKF_1338  | <i>ynaC</i>  | Multidrug/protein/lipid ABC transporter family, ATP-binding and permease protein | -0.370         | -1.543         | 0.071          | -2.178       | -0.234           | 0.615          | 0.036          | 0.947          | 0.000        | 0.593            | 2       |
| LLKF_1406  | <i>mtsC</i>  | Manganese ABC transporter, permease protein                                      | 0.876          | 0.405          | 0.696          | -2.179       | -0.226           | 0.252          | 0.595          | 0.330          | 0.000        | 0.645            | 2       |
| LLKF_1420  | <i>yngF</i>  | Nucleoside ABC transporter, permease protein                                     | -0.307         | -0.525         | 0.106          | -2.067       | -0.434           | 0.682          | 0.448          | 0.916          | 0.000        | 0.348            | 2       |
| LLKF_1421  | <i>yngG</i>  | Nucleoside ABC transporter, permease protein                                     | -0.536         | -0.661         | 0.072          | -2.393       | -0.591           | 0.405          | 0.310          | 0.902          | 0.000        | 0.136            | 2       |
| LLKF_1463  | <i>yobA</i>  | Universal stress protein family protein                                          | -0.462         | 0.257          | 0.507          | -2.874       | -0.114           | 0.593          | 0.771          | 0.590          | 0.000        | 0.512            | 2       |
| LLKF_1544  | <i>bmpA</i>  | Basic membrane lipoprotein                                                       | -0.289         | -0.659         | 0.153          | -1.767       | 0.061            | 0.704          | 0.342          | 0.737          | 0.001        | 0.639            | 2       |
| LLKF_1564  | <i>ptbA</i>  | PTS system, beta-glucoside-specific IIA component                                | -1.311         | -1.237         | -0.433         | -2.427       | 0.127            | 0.196          | 0.233          | 0.689          | 0.000        | 0.849            | 2       |
| LLKF_1565  | <i>bglR</i>  | Transcription antiterminator, BglG family                                        | -1.891         | -1.595         | -0.517         | -2.304       | 0.009            | 0.087          | 0.131          | 0.651          | 0.001        | 0.945            | 2       |
| LLKF_1578  | <i>yjaD</i>  | Hypothetical protein                                                             | 2.169          | 0.470          | 1.715          | -2.192       | 0.446            | 0.020          | 0.562          | 0.027          | 0.001        | 0.362            | 2       |
| LLKF_1579  | <i>yjaE</i>  | Hypothetical protein                                                             | 1.772          | 0.156          | 1.559          | -2.168       | 0.091            | 0.035          | 0.776          | 0.017          | 0.000        | 0.810            | 2       |
| LLKF_1602  | <i>glcK</i>  | Glucokinase / transcription regulator. ROK family                                | -1.041         | -1.789         | 0.107          | -2.194       | -0.156           | 0.229          | 0.039          | 0.926          | 0.001        | 0.471            | 2       |
| LLKF_1607  | <i>lnbA</i>  | Lacto-N-biosidase                                                                | -1.103         | -1.966         | -0.258         | -1.787       | -0.160           | 0.169          | 0.020          | 0.803          | 0.001        | 0.759            | 2       |
| LLKF_1736  | <i>yqcG</i>  | Hypothetical protein                                                             | -0.267         | -0.110         | -0.232         | -2.280       | -0.881           | 0.657          | 0.868          | 0.735          | 0.000        | 0.024            | 2       |
| LLKF_1817  | <i>eutD</i>  | Phosphate acetyltransferase                                                      | -1.182         | -1.253         | -0.749         | -1.995       | -0.264           | 0.187          | 0.190          | 0.348          | 0.000        | 0.232            | 2       |
| LLKF_1844  | <i>malG</i>  | Maltose ABC transporter, permease protein                                        | -1.286         | -1.431         | -0.485         | -1.817       | -0.508           | 0.125          | 0.071          | 0.538          | 0.001        | 0.453            | 2       |
| LLKF_1863  |              | Transcriptional regulator, LuxR family                                           | 0.018          | -0.119         | -0.112         | -1.593       | 0.170            | 0.982          | 0.877          | 0.904          | 0.000        | 0.677            | 2       |
| LLKF_1868  | <i>ptnAB</i> | Mannose-specific PTS system, IIA component                                       | -0.644         | -0.517         | -0.507         | -1.786       | 0.636            | 0.425          | 0.513          | 0.460          | 0.001        | 0.188            | 2       |
| LLKF_1869  | <i>ptnC</i>  | Mannose-specific PTS system, IIC component                                       | -0.593         | -0.454         | -0.513         | -2.054       | 0.418            | 0.441          | 0.552          | 0.502          | 0.000        | 0.422            | 2       |
| LLKF_1935  | <i>atpC</i>  | ATP synthase F1, epsilon subunit                                                 | 0.859          | 1.070          | 0.382          | -2.120       | 0.337            | 0.229          | 0.129          | 0.574          | 0.000        | 0.306            | 2       |
| LLKF_1943  | <i>estA</i>  | Tributyryl esterase                                                              | -0.552         | -0.171         | 0.497          | -1.455       | -0.145           | 0.335          | 0.795          | 0.364          | 0.000        | 0.695            | 2       |

| Feature ID | Gene             | Annotation                                                                                     | NZ5521_<br>log | NZ5522_<br>log | NZ5523_<br>log | IL594_<br>og | KF147prt_<br>log | NZ5521_<br>log | NZ5522_<br>log | NZ5523_<br>log | IL594_<br>og | KF147prt_<br>log | cluster |
|------------|------------------|------------------------------------------------------------------------------------------------|----------------|----------------|----------------|--------------|------------------|----------------|----------------|----------------|--------------|------------------|---------|
| LLKF_1980  |                  | Hypothetical protein                                                                           | -0.349         | -1.510         | -0.683         | -3.341       | -0.325           | 0.699          | 0.076          | 0.405          | 0.000        | 0.530            | 2       |
| LLKF_2034  | <i>rplT</i>      | LSU ribosomal protein L20P                                                                     | 1.314          | 0.619          | -0.938         | -1.993       | 1.265            | 0.086          | 0.414          | 0.156          | 0.001        | 0.016            | 2       |
| LLKF_2047  | <i>ytcb</i>      | Hypothetical protein                                                                           | 0.024          | -0.073         | 0.053          | -1.625       | -0.797           | 0.930          | 0.938          | 0.962          | 0.001        | 0.074            | 2       |
| LLKF_2049  | <i>ytcc</i>      | Hypothetical protein                                                                           | 0.231          | -0.281         | 0.195          | -3.190       | 1.306            | 0.788          | 0.734          | 0.850          | 0.000        | 0.020            | 2       |
| LLKF_2093  | <i>ytgF</i>      | 2',3'-cyclic-nucleotide 2'-phosphodiesterase                                                   | -0.850         | -0.798         | -0.861         | -1.745       | -0.286           | 0.266          | 0.284          | 0.195          | 0.001        | 0.376            | 2       |
| LLKF_2110  | <i>cblA/cglA</i> | Cystathionine beta-lyase                                                                       | -0.095         | -0.459         | 0.045          | -2.073       | -2.343           | 0.857          | 0.519          | 0.951          | 0.000        | 0.000            | 2       |
| LLKF_2111  | <i>cgs</i>       | Cystathionine gamma-synthase                                                                   | 0.241          | -0.304         | 0.198          | -2.244       | -2.181           | 0.752          | 0.574          | 0.803          | 0.000        | 0.001            | 2       |
| LLKF_2129  | <i>purA</i>      | Adenylosuccinate synthetase                                                                    | 0.891          | 0.067          | 0.450          | -1.802       | 1.501            | 0.316          | 0.645          | 0.544          | 0.001        | 0.013            | 2       |
| LLKF_2171  | <i>yugB</i>      | Aldo/keto reductase                                                                            | -0.262         | -1.476         | 0.365          | -3.967       | 0.404            | 0.749          | 0.056          | 0.670          | 0.000        | 0.376            | 2       |
| LLKF_2187  | <i>rplA</i>      | LSU ribosomal protein L1P                                                                      | -0.184         | -0.309         | -0.219         | -2.406       | 0.041            | 0.785          | 0.658          | 0.761          | 0.000        | 0.775            | 2       |
| LLKF_2188  | <i>rplK</i>      | LSU ribosomal protein L11P                                                                     | 0.945          | -0.040         | -0.249         | -2.442       | 0.666            | 0.211          | 0.947          | 0.739          | 0.000        | 0.140            | 2       |
| LLKF_2198  | <i>ackA2</i>     | Acetate kinase                                                                                 | -1.212         | -0.317         | -0.101         | -2.987       | -0.689           | 0.154          | 0.722          | 0.914          | 0.000        | 0.278            | 2       |
| LLKF_2224  | <i>argS</i>      | Arginyl-tRNA synthetase                                                                        | 0.056          | -0.229         | -0.092         | -1.516       | 0.434            | 0.632          | 0.621          | 0.841          | 0.000        | 0.338            | 2       |
| LLKF_2329  | <i>rpmD</i>      | LSU ribosomal protein L30P                                                                     | -0.037         | -0.026         | -0.659         | -2.232       | 0.325            | 0.923          | 0.812          | 0.205          | 0.000        | 0.353            | 2       |
| LLKF_2330  | <i>rpsE</i>      | SSU ribosomal protein S5P                                                                      | 0.248          | 0.276          | -0.225         | -2.148       | 0.734            | 0.714          | 0.415          | 0.789          | 0.000        | 0.143            | 2       |
| LLKF_2331  | <i>rplR</i>      | LSU ribosomal protein L18P                                                                     | 0.146          | 0.327          | -0.433         | -2.463       | 0.518            | 0.620          | 0.628          | 0.512          | 0.000        | 0.220            | 2       |
| LLKF_2332  | <i>rplF</i>      | LSU ribosomal protein L6P                                                                      | 0.895          | 1.089          | -0.173         | -2.487       | 0.849            | 0.159          | 0.089          | 0.827          | 0.000        | 0.039            | 2       |
| LLKF_2333  | <i>rpsH</i>      | SSU ribosomal protein S8P                                                                      | 0.845          | 1.257          | 0.149          | -2.080       | 1.198            | 0.307          | 0.088          | 0.891          | 0.001        | 0.023            | 2       |
| LLKF_2335  | <i>rpsN</i>      | SSU ribosomal protein S14P                                                                     | 1.479          | 1.179          | 0.234          | -1.678       | 0.742            | 0.032          | 0.066          | 0.739          | 0.000        | 0.064            | 2       |
| LLKF_2336  | <i>rplE</i>      | LSU ribosomal protein L5P                                                                      | 1.170          | 1.216          | 0.138          | -1.971       | 0.792            | 0.084          | 0.061          | 0.871          | 0.000        | 0.057            | 2       |
| LLKF_2337  | <i>rplX</i>      | LSU ribosomal protein L24P                                                                     | 1.078          | 0.927          | 0.063          | -2.085       | 0.778            | 0.178          | 0.241          | 0.925          | 0.000        | 0.093            | 2       |
| LLKF_2338  | <i>rplN</i>      | LSU ribosomal protein L14P                                                                     | 1.488          | 1.233          | 0.374          | -3.405       | 0.848            | 0.042          | 0.069          | 0.590          | 0.000        | 0.045            | 2       |
| LLKF_2339  | <i>rpsQ</i>      | SSU ribosomal protein S17P                                                                     | 1.498          | 1.266          | 0.216          | -3.397       | 0.953            | 0.079          | 0.125          | 0.709          | 0.000        | 0.097            | 2       |
| LLKF_2340  | <i>rpmC</i>      | LSU ribosomal protein L29P                                                                     | 1.782          | 1.616          | 0.345          | -3.311       | 1.043            | 0.035          | 0.058          | 0.654          | 0.000        | 0.062            | 2       |
| LLKF_2341  | <i>rplP</i>      | LSU ribosomal protein L16P                                                                     | 1.256          | 1.407          | 0.155          | -3.272       | 0.960            | 0.082          | 0.049          | 0.855          | 0.000        | 0.059            | 2       |
| LLKF_2342  | <i>rpsC</i>      | SSU ribosomal protein S3P                                                                      | 1.161          | 1.353          | 0.288          | -3.103       | 1.274            | 0.079          | 0.038          | 0.693          | 0.000        | 0.009            | 2       |
| LLKF_2343  | <i>rplV</i>      | LSU ribosomal protein L22P                                                                     | 1.870          | 1.498          | 0.220          | -3.365       | 1.230            | 0.015          | 0.027          | 0.778          | 0.000        | 0.010            | 2       |
| LLKF_2344  | <i>rpsS</i>      | SSU ribosomal protein S19P                                                                     | 1.837          | 1.375          | 0.282          | -3.562       | 0.789            | 0.023          | 0.086          | 0.679          | 0.000        | 0.100            | 2       |
| LLKF_2345  | <i>rplB</i>      | LSU ribosomal protein L2P                                                                      | 0.641          | 0.644          | -0.144         | -2.776       | 0.552            | 0.365          | 0.389          | 0.847          | 0.000        | 0.270            | 2       |
| LLKF_2346  | <i>rplW</i>      | LSU ribosomal protein L23P                                                                     | 0.894          | 0.820          | -0.293         | -3.396       | 0.653            | 0.200          | 0.225          | 0.690          | 0.000        | 0.115            | 2       |
| LLKF_2347  | <i>rplD</i>      | LSU ribosomal protein L1E (= L4P)                                                              | 0.822          | 0.691          | -0.251         | -3.102       | 0.910            | 0.254          | 0.310          | 0.758          | 0.000        | 0.042            | 2       |
| LLKF_2348  | <i>rplC</i>      | LSU ribosomal protein L3P                                                                      | 0.551          | 0.568          | -0.534         | -3.450       | 0.886            | 0.385          | 0.371          | 0.374          | 0.000        | 0.035            | 2       |
| LLKF_2349  | <i>rpsJ</i>      | SSU ribosomal protein S10P                                                                     | 1.029          | 0.861          | -0.069         | -2.911       | 1.005            | 0.138          | 0.197          | 0.923          | 0.000        | 0.032            | 2       |
| LLKF_2381  | <i>yajC</i>      | Protein translocase subunit YajC                                                               | -1.101         | -0.773         | -0.829         | -1.765       | -0.880           | 0.103          | 0.232          | 0.158          | 0.000        | 0.042            | 2       |
| LLKF_2395  | <i>tsf</i>       | Translation elongation factor Ts (EF-Ts)                                                       | -0.215         | 0.196          | -0.345         | -2.364       | -0.306           | 0.829          | 0.851          | 0.750          | 0.000        | 0.576            | 2       |
| LLKF_2396  | <i>rpsB</i>      | SSU ribosomal protein S2P                                                                      | 0.273          | 0.570          | -0.180         | -1.979       | -0.111           | 0.671          | 0.369          | 0.654          | 0.000        | 0.644            | 2       |
| LLKF_2402  | <i>ywdD</i>      | Bifunctional protein: Fe-S oxidoreductase, radical SAM superfamily/transporter, MF superfamily | 0.229          | -0.764         | -0.226         | -2.250       | -0.667           | 0.749          | 0.288          | 0.769          | 0.001        | 0.201            | 2       |
| LLKF_2433  | <i>ywhB</i>      | Metallo-phosphoesterase                                                                        | -0.247         | -0.284         | -0.716         | -1.465       | -0.415           | 0.720          | 0.689          | 0.240          | 0.001        | 0.448            | 2       |

| Feature ID | Gene         | Annotation                                                            | NZ5521_<br>log | NZ5522_<br>log | NZ5523_<br>log | IL594_<br>og | KF147prt_<br>log | NZ5521_<br>log | NZ5522_<br>log | NZ5523_<br>log | IL594_<br>og | KF147prt_<br>log | cluster |
|------------|--------------|-----------------------------------------------------------------------|----------------|----------------|----------------|--------------|------------------|----------------|----------------|----------------|--------------|------------------|---------|
| LLKF_2434  | <i>rpsR</i>  | SSU ribosomal protein S18P                                            | 0.529          | -0.271         | -0.679         | -1.556       | 0.638            | 0.470          | 0.475          | 0.295          | 0.001        | 0.147            | 2       |
| LLKF_2436  | <i>rpsF</i>  | SSU ribosomal protein S6P                                             | 1.411          | 0.592          | -0.561         | -1.649       | 1.186            | 0.049          | 0.371          | 0.382          | 0.001        | 0.031            | 2       |
| LLKF_2496  | <i>usp45</i> | Hypothetical protein, secreted                                        | 0.765          | 0.562          | 0.013          | -1.742       | -0.272           | 0.306          | 0.453          | 0.860          | 0.001        | 0.552            | 2       |
| LLKF_2505  | <i>ycxA</i>  | Activator of (R)-2-hydroxyglutaryl-CoA dehydratase                    | -0.941         | -1.127         | -0.188         | -2.181       | -1.217           | 0.295          | 0.197          | 0.809          | 0.000        | 0.021            | 2       |
| LLKF_2521  | <i>rplM</i>  | LSU ribosomal protein L13P                                            | 0.687          | 0.658          | -0.415         | -1.700       | 0.659            | 0.295          | 0.313          | 0.523          | 0.000        | 0.179            | 2       |
| LLKF_2528  | <i>rpsG</i>  | SSU ribosomal protein S7P                                             | 0.352          | 0.181          | -0.430         | -1.616       | 0.388            | 0.507          | 0.458          | 0.559          | 0.001        | 0.418            | 2       |
| LLKF_2529  | <i>rpsL</i>  | SSU ribosomal protein S12P                                            | 1.260          | 0.847          | -0.208         | -1.589       | 0.931            | 0.055          | 0.161          | 0.775          | 0.000        | 0.028            | 2       |
| LLKF_0052  | <i>cysD</i>  | O-acetyl-L-homoserine sulfhydrylase / O-acetyl-L-serine sulfhydrylase | -2.666         | -1.921         | -2.525         | -2.241       | -4.428           | 0.004          | 0.014          | 0.002          | 0.000        | 0.000            | 3       |
| LLKF_0165  | <i>ybhD</i>  | Acetyltransferase, GNAT family                                        | -1.793         | -1.839         | -0.532         | -3.329       | 0.199            | 0.033          | 0.023          | 0.486          | 0.000        | 0.687            | 3       |
| LLKF_0168  |              | Hypothetical protein                                                  | -3.262         | -3.255         | -0.255         | -3.265       | -2.411           | 0.002          | 0.001          | 0.668          | 0.000        | 0.001            | 3       |
| LLKF_0169  |              | Hypothetical protein                                                  | -2.915         | -3.324         | -0.717         | -3.241       | -2.556           | 0.008          | 0.003          | 0.433          | 0.000        | 0.002            | 3       |
| LLKF_0170  | <i>bglS</i>  | 6-Phospho-beta-glucosidase                                            | -1.682         | -2.583         | 0.178          | -4.713       | -0.742           | 0.080          | 0.012          | 0.878          | 0.000        | 0.194            | 3       |
| LLKF_0466  | <i>ptcA</i>  | PTS system, cellobiose-specific IIA component                         | -2.926         | -2.740         | -0.435         | -4.725       | -0.457           | 0.012          | 0.011          | 0.639          | 0.000        | 0.406            | 3       |
| LLKF_0467  | <i>yecA</i>  | Transcriptional regulator, RpiR family                                | -1.527         | -1.638         | -0.271         | -4.045       | -0.270           | 0.229          | 0.193          | 0.880          | 0.000        | 0.743            | 3       |
| LLKF_0714  | <i>ygjD</i>  | 4-Alpha-glucanotransferase                                            | -1.956         | -2.220         | -1.015         | -2.880       | 0.275            | 0.075          | 0.037          | 0.237          | 0.000        | 0.641            | 3       |
| LLKF_0924  | <i>butB</i>  | (R,R)-butanediol dehydrogenase                                        | -2.837         | -2.863         | -0.900         | -2.725       | 0.555            | 0.030          | 0.026          | 0.444          | 0.001        | 0.485            | 3       |
| LLKF_0986  | <i>fruR</i>  | Fructose/lactose transport transcriptional regulator, DeoR family     | -3.564         | -4.448         | -1.613         | -3.225       | -0.002           | 0.008          | 0.002          | 0.112          | 0.000        | 0.998            | 3       |
| LLKF_0987  | <i>fruB</i>  | 1-phosphofructokinase                                                 | -4.155         | -4.366         | -1.243         | -3.419       | 0.104            | 0.009          | 0.003          | 0.199          | 0.000        | 0.799            | 3       |
| LLKF_0988  | <i>fruA</i>  | PTS system, fructose-specific IIA component                           | -4.106         | -4.702         | -0.963         | -3.914       | -0.484           | 0.004          | 0.001          | 0.336          | 0.000        | 0.526            | 3       |
| LLKF_1601  | <i>fruK</i>  | Fructokinase                                                          | -1.669         | -2.326         | -0.002         | -3.165       | -0.812           | 0.045          | 0.008          | 0.946          | 0.000        | 0.089            | 3       |
| LLKF_1603  | <i>ypcA</i>  | Beta-glucosidase                                                      | -1.343         | -1.831         | 0.027          | -2.723       | -0.184           | 0.124          | 0.050          | 0.930          | 0.000        | 0.697            | 3       |
| LLKF_1604  | <i>ypcB</i>  | Hypothetical protein                                                  | -1.735         | -1.877         | -0.220         | -2.884       | -0.306           | 0.032          | 0.020          | 0.814          | 0.000        | 0.468            | 3       |
| LLKF_1606  | <i>dexB</i>  | Glucan 1,6-alpha-glucosidase                                          | -1.557         | -2.168         | -0.412         | -2.855       | -0.050           | 0.107          | 0.029          | 0.711          | 0.000        | 0.711            | 3       |
| LLKF_1610  | <i>ypdA</i>  | Sugar ABC transporter, permease protein                               | -2.375         | -3.432         | 0.175          | -4.658       | -1.134           | 0.036          | 0.007          | 0.865          | 0.000        | 0.061            | 3       |
| LLKF_1784  | <i>kdgK2</i> | 2-dehydro-3-deoxygluconokinase                                        | -2.913         | -3.179         | -1.732         | -3.168       | -2.755           | 0.004          | 0.003          | 0.012          | 0.000        | 0.001            | 3       |
| LLKF_1785  | <i>uxaC</i>  | Uronate isomerase                                                     | -2.429         | -3.082         | -1.780         | -2.700       | -1.941           | 0.038          | 0.004          | 0.019          | 0.000        | 0.046            | 3       |
| LLKF_1786  | <i>yqhA</i>  | Aldose 1-epimerase family protein , C-terminal fragment               | -2.626         | -2.980         | -1.839         | -2.863       | -2.248           | 0.004          | 0.002          | 0.007          | 0.000        | 0.001            | 3       |
| LLKF_1787  | <i>uxuT</i>  | D-glucuronate transporter                                             | -2.357         | -2.476         | -1.690         | -2.882       | -1.761           | 0.021          | 0.012          | 0.049          | 0.000        | 0.009            | 3       |
| LLKF_1789  | <i>uxuB</i>  | Fructuronate reductase                                                | -3.003         | -2.543         | -2.039         | -1.757       | -2.384           | 0.003          | 0.004          | 0.005          | 0.001        | 0.001            | 3       |
| LLKF_1809  | <i>yraA</i>  | Hypothetical protein                                                  | -1.339         | -1.488         | -1.573         | -3.087       | -2.612           | 0.277          | 0.235          | 0.125          | 0.000        | 0.006            | 3       |
| LLKF_1830  | <i>arb</i>   | 6-phospho-beta-glucosidase                                            | -3.059         | -2.723         | -0.466         | -2.631       | -0.970           | 0.005          | 0.007          | 0.595          | 0.000        | 0.086            | 3       |
| LLKF_1842  | <i>malE</i>  | Maltose ABC transporter, substrate binding protein                    | -2.677         | -3.030         | -1.190         | -2.981       | -0.481           | 0.003          | 0.001          | 0.045          | 0.000        | 0.265            | 3       |
| LLKF_1981  | <i>adhA</i>  | Alcohol dehydrogenase 1                                               | -2.054         | -1.848         | -0.831         | -4.200       | -0.101           | 0.115          | 0.123          | 0.436          | 0.000        | 0.733            | 3       |
| LLKF_2197  | <i>yuiE</i>  | Hypothetical protein                                                  | -2.056         | -1.975         | -0.404         | -3.273       | -0.374           | 0.052          | 0.058          | 0.735          | 0.000        | 0.548            | 3       |
| LLKF_2219  | <i>arcC2</i> | Carbamate kinase                                                      | -2.452         | -2.737         | -0.954         | -3.680       | -1.684           | 0.004          | 0.002          | 0.106          | 0.000        | 0.003            | 3       |
| LLKF_2220  | <i>arcC1</i> | Carbamate kinase                                                      | -2.204         | -2.644         | -0.650         | -3.485       | -1.927           | 0.010          | 0.003          | 0.341          | 0.000        | 0.002            | 3       |
| LLKF_2221  | <i>arcD1</i> | Arginine/ornithine antiporter                                         | -1.597         | -2.253         | -0.503         | -2.996       | -1.298           | 0.066          | 0.014          | 0.523          | 0.000        | 0.021            | 3       |

| Feature ID | Gene         | Annotation                                                            | NZ5521_<br>log | NZ5522_<br>log | NZ5523_<br>log | IL594_<br>og | KF147prt_<br>log | NZ5521_<br>log | NZ5522_<br>log | NZ5523_<br>log | IL594_<br>og | KF147prt_<br>log | cluster |
|------------|--------------|-----------------------------------------------------------------------|----------------|----------------|----------------|--------------|------------------|----------------|----------------|----------------|--------------|------------------|---------|
| LLKF_2222  | <i>arcB</i>  | Ornithine carbamoyltransferase                                        | -2.366         | -2.876         | -0.897         | -3.651       | -1.762           | 0.008          | 0.002          | 0.154          | 0.000        | 0.005            | 3       |
| LLKF_2223  | <i>arcA</i>  | Arginine deiminase                                                    | -2.084         | -2.339         | -0.735         | -3.203       | -0.709           | 0.011          | 0.005          | 0.263          | 0.000        | 0.105            | 3       |
| LLKF_0166  | <i>ybhE</i>  | Hypothetical protein                                                  | -3.666         | -3.486         | -0.344         | -5.634       | -1.179           | 0.008          | 0.007          | 0.753          | 0.000        | 0.085            | 4       |
| LLKF_0167  | <i>celB</i>  | PTS system, cellobiose-specific IIC component                         | -3.334         | -4.203         | 0.026          | -6.959       | -1.183           | 0.005          | 0.001          | 0.824          | 0.000        | 0.110            | 4       |
| LLKF_0280  | <i>ymgG</i>  | General stress protein, Gls24 family                                  | 1.285          | -3.813         | -1.733         | -5.816       | -0.372           | 0.198          | 0.002          | 0.047          | 0.000        | 0.544            | 4       |
| LLKF_0465  | <i>ptcB</i>  | PTS system, cellobiose-specific IIB component                         | -3.498         | -3.411         | -0.429         | -5.722       | -1.260           | 0.002          | 0.001          | 0.603          | 0.000        | 0.017            | 4       |
| LLKF_0473  | <i>msmK</i>  | Multiple sugar ABC transporter, ATP-binding protein MsmK              | -3.169         | -3.881         | -0.758         | -5.184       | -0.994           | 0.024          | 0.010          | 0.528          | 0.000        | 0.190            | 4       |
| LLKF_1319  | <i>metF</i>  | Methylenetetrahydrofolate reductase                                   | -1.242         | -2.021         | -0.442         | -6.900       | -4.865           | 0.193          | 0.039          | 0.674          | 0.000        | 0.000            | 4       |
| LLKF_1320  | <i>metE</i>  | 5-methyltetrahydropteroyltryglutamate--homocysteine methyltransferase | -1.806         | -2.165         | -0.704         | -6.921       | -5.012           | 0.087          | 0.043          | 0.479          | 0.000        | 0.000            | 4       |
| LLKF_1608  | <i>ypcG</i>  | Sugar ABC transporter, substrate-binding protein                      | -3.425         | -4.097         | -0.345         | -5.939       | -1.442           | 0.014          | 0.007          | 0.795          | 0.000        | 0.066            | 4       |
| LLKF_1609  | <i>ypcH</i>  | Sugar ABC transporter, permease protein                               | -2.827         | -3.672         | 0.156          | -4.964       | -1.495           | 0.019          | 0.003          | 0.858          | 0.000        | 0.029            | 4       |
| LLKF_1611  | <i>ypdB</i>  | Alpha-mannosidase                                                     | -3.111         | -3.934         | -0.304         | -5.291       | -1.624           | 0.020          | 0.005          | 0.817          | 0.000        | 0.029            | 4       |
| LLKF_1612  | <i>ypdC</i>  | Hypothetical protein                                                  | -3.115         | -4.103         | -0.757         | -4.883       | -1.342           | 0.011          | 0.002          | 0.416          | 0.000        | 0.047            | 4       |
| LLKF_2163  | <i>galE</i>  | UDP-glucose 4-epimerase                                               | -2.352         | -3.382         | 0.228          | -5.841       | -1.261           | 0.006          | 0.000          | 0.763          | 0.000        | 0.012            | 4       |
| LLKF_2164  | <i>lacZ</i>  | Beta-galactosidase                                                    | -1.797         | -2.984         | 0.304          | -7.560       | -0.707           | 0.065          | 0.003          | 0.705          | 0.000        | 0.147            | 4       |
| LLKF_2165  | <i>thgA</i>  | Galactoside O-acetyltransferase                                       | -1.716         | -3.220         | 0.706          | -7.226       | -0.363           | 0.029          | 0.001          | 0.225          | 0.000        | 0.393            | 4       |
| LLKF_2166  | <i>galT1</i> | Galactose-1-phosphate uridylyltransferase                             | -0.979         | -3.049         | 0.671          | -6.983       | -0.192           | 0.275          | 0.003          | 0.382          | 0.000        | 0.579            | 4       |
| LLKF_2167  | <i>galK1</i> | Galactokinase                                                         | -1.626         | -3.625         | 0.397          | -7.171       | -0.501           | 0.056          | 0.001          | 0.646          | 0.000        | 0.407            | 4       |
| LLKF_2168  | <i>galM1</i> | Aldose 1-epimerase                                                    | -2.087         | -3.702         | 0.662          | -7.782       | -0.691           | 0.008          | 0.000          | 0.293          | 0.000        | 0.140            | 4       |
| LLKF_2169  | <i>lacS</i>  | Lactose permease                                                      | -2.398         | -3.484         | 0.240          | -7.408       | -0.229           | 0.006          | 0.001          | 0.695          | 0.000        | 0.259            | 4       |
| LLKF_0372  | <i>plpA</i>  | ABC transporter, substrate-binding protein, NLPA lipofamily           | -1.635         | 0.652          | -0.309         | -1.554       | -3.999           | 0.095          | 0.493          | 0.636          | 0.003        | 0.000            | 5       |
| LLKF_0373  | <i>plpB</i>  | ABC transporter, substrate-binding protein, NLPA lipofamily           | -1.489         | 0.392          | -0.374         | -1.411       | -4.675           | 0.113          | 0.695          | 0.715          | 0.011        | 0.000            | 5       |
| LLKF_0374  | <i>plpC</i>  | ABC transporter, substrate-binding protein, NLPA lipofamily           | -1.166         | 0.579          | -0.057         | -1.348       | -4.688           | 0.207          | 0.548          | 0.955          | 0.011        | 0.000            | 5       |
| LLKF_0375  | <i>plpD</i>  | ABC transporter, substrate-binding protein, NLPA lipofamily           | -0.674         | 0.965          | 0.157          | -1.104       | -4.258           | 0.508          | 0.293          | 0.882          | 0.012        | 0.000            | 5       |
| LLKF_0376  | <i>ycdB</i>  | ABC transporter, ATP-binding protein                                  | -0.800         | 0.786          | -0.077         | -1.545       | -3.924           | 0.343          | 0.359          | 0.725          | 0.003        | 0.000            | 5       |
| LLKF_0377  | <i>ycdC</i>  | ABC transporter, permease protein                                     | -0.833         | 0.921          | 0.046          | -1.285       | -3.848           | 0.352          | 0.292          | 0.927          | 0.012        | 0.000            | 5       |
| LLKF_0378  | <i>cbiQ1</i> | ABC-type cobalt transporter, permease protein CbiQ                    | -0.942         | 0.667          | -0.051         | -1.325       | -3.262           | 0.196          | 0.397          | 0.924          | 0.004        | 0.000            | 5       |
| LLKF_0965  | <i>yjgC</i>  | Amino acid ABC transporter, substrate-binding protein                 | -0.801         | -1.075         | -1.297         | -0.326       | -2.090           | 0.260          | 0.091          | 0.026          | 0.319        | 0.001            | 5       |
| LLKF_1351  | <i>gltD</i>  | Glutamate synthase [NADPH], small chain                               | -0.368         | -2.684         | -0.857         | 1.921        | -1.109           | 0.637          | 0.003          | 0.199          | 0.000        | 0.041            | 5       |
| LLKF_1352  | <i>gltB</i>  | Glutamate synthase [NADPH], large chain                               | -0.348         | -2.025         | -0.228         | 2.133        | -0.655           | 0.656          | 0.019          | 0.773          | 0.000        | 0.173            | 5       |
| LLKF_1885  | <i>yrjI</i>  | Phosphoglycerate mutase family protein                                | 0.039          | -0.308         | 0.168          | 0.713        | -1.994           | 0.960          | 0.640          | 0.842          | 0.032        | 0.001            | 5       |
| LLKF_0421  | <i>lysQ</i>  | Lysine-specific permease                                              | 4.542          | 1.136          | 3.019          | 0.095        | 0.107            | 0.001          | 0.208          | 0.001          | 0.774        | 0.813            | 6       |
| LLKF_1260  | <i>leuA</i>  | 2-isopropylmalate synthase                                            | 3.644          | -0.657         | 1.967          | 4.198        | -0.752           | 0.003          | 0.449          | 0.014          | 0.000        | 0.175            | 6       |

| Feature ID | Gene         | Annotation                                                      | NZ5521_<br>log | NZ5522_<br>log | NZ5523_<br>log | IL594_<br>og | KF147prt_<br>log | NZ5521_<br>log | NZ5522_<br>log | NZ5523_<br>log | IL594_<br>og | KF147prt_<br>log | cluster |
|------------|--------------|-----------------------------------------------------------------|----------------|----------------|----------------|--------------|------------------|----------------|----------------|----------------|--------------|------------------|---------|
| LLKF_1261  | <i>leuB</i>  | 3-isopropylmalate dehydrogenase                                 | 3.165          | -0.944         | 1.973          | 4.063        | -0.713           | 0.008          | 0.351          | 0.029          | 0.000        | 0.256            | 6       |
| LLKF_1263  | <i>leuC</i>  | 3-isopropylmalate dehydratase, large subunit                    | 3.677          | -0.663         | 2.128          | 3.958        | -0.726           | 0.006          | 0.528          | 0.032          | 0.000        | 0.367            | 6       |
| LLKF_1264  | <i>leuD</i>  | 3-isopropylmalate dehydratase, small subunit                    | 3.401          | -0.817         | 2.118          | 4.120        | -0.946           | 0.018          | 0.531          | 0.058          | 0.000        | 0.217            | 6       |
| LLKF_1265  | <i>ymeB</i>  | ABC transporter, ATP-binding protein                            | 3.313          | -0.651         | 2.277          | 4.062        | -0.728           | 0.094          | 0.723          | 0.109          | 0.001        | 0.457            | 6       |
| LLKF_1266  | <i>ilvD</i>  | Dihydroxy-acid dehydratase                                      | 3.220          | -0.999         | 1.434          | 3.625        | -0.581           | 0.009          | 0.344          | 0.120          | 0.000        | 0.356            | 6       |
| LLKF_1267  | <i>ilvB</i>  | Acetolactate synthase, large subunit                            | 2.975          | -0.922         | 1.426          | 3.647        | -0.738           | 0.008          | 0.338          | 0.088          | 0.000        | 0.202            | 6       |
| LLKF_1268  | <i>ilvH</i>  | Acetolactate synthase, small subunit                            | 3.075          | -0.925         | 1.352          | 3.418        | -0.672           | 0.028          | 0.413          | 0.184          | 0.000        | 0.333            | 6       |
| LLKF_1269  | <i>ilvC</i>  | Ketol-acid reductoisomerase                                     | 3.075          | -0.823         | 1.391          | 3.535        | -0.356           | 0.030          | 0.408          | 0.102          | 0.000        | 0.578            | 6       |
| LLKF_2029  | <i>oppA</i>  | Oligopeptide ABC transporter, oligopeptide-binding protein OppA | 5.416          | 5.110          | 0.135          | 2.820        | 0.248            | 0.001          | 0.000          | 0.824          | 0.000        | 0.679            | 7       |
| LLKF_2031  | <i>oppB</i>  | Oligopeptide ABC transporter, permease protein OppB             | 4.899          | 4.564          | 0.003          | 8.400        | -0.158           | 0.003          | 0.003          | 0.999          | 0.000        | 0.856            | 7       |
| LLKF_2032  | <i>oppF</i>  | Oligopeptide ABC transporter, ATP-binding protein OppF          | 5.068          | 4.718          | -0.124         | 8.176        | -0.228           | 0.003          | 0.002          | 0.946          | 0.000        | 0.777            | 7       |
| LLKF_2033  | <i>oppD</i>  | Oligopeptide ABC transporter, ATP-binding protein OppD          | 4.698          | 4.355          | -0.195         | 8.122        | -0.087           | 0.003          | 0.003          | 0.896          | 0.000        | 0.885            | 7       |
| LLKF_2273  |              | IS981 transposase B                                             | 0.634          | -0.701         | -1.676         | 4.488        | 1.212            | 0.579          | 0.521          | 0.098          | 0.000        | 0.075            | 8       |
| LLKF_2274  |              | IS981 transposase A                                             | 0.818          | -0.692         | -2.683         | 4.709        | 2.090            | 0.490          | 0.579          | 0.013          | 0.000        | 0.019            | 8       |
| LLKF_2276  |              | IS981 transposase B                                             | 0.634          | -0.701         | -1.676         | 4.488        | 1.212            | 0.579          | 0.521          | 0.098          | 0.000        | 0.075            | 8       |
| LLKF_2277  |              | IS981 transposase A                                             | 0.818          | -0.692         | -2.683         | 4.709        | 2.090            | 0.490          | 0.579          | 0.013          | 0.000        | 0.019            | 8       |
| LLKF_2426  | <i>ywfG</i>  | Mucus-binding protein, LPXTG-anchored                           | 0.263          | 0.359          | -0.022         | 7.502        | 0.417            | 0.690          | 0.676          | 0.671          | 0.000        | 0.566            | 8       |
| LLKF_2502  | <i>yxbD</i>  | Transporter, MFS superfamily                                    | 0.805          | 3.454          | 0.151          | 5.679        | 4.780            | 0.456          | 0.004          | 0.799          | 0.000        | 0.000            | 9       |
| LLKF_2503  | <i>uspA4</i> | Universal stress protein A                                      | 1.547          | 4.861          | 0.352          | 6.633        | 5.886            | 0.139          | 0.001          | 0.717          | 0.000        | 0.000            | 9       |
| LLKF_2504  | <i>yxbF</i>  | Hypothetical protein                                            | 1.396          | 4.830          | 0.453          | 6.773        | 5.920            | 0.231          | 0.002          | 0.727          | 0.000        | 0.000            | 9       |

### Supplemental Table 4

Transcriptome data from stationary cells as compared to KF147. Selected genes show significant differential regulation ( $p < 0.001$ ) in at least one of the samples. This dataset was used for the generation of Supplemental Figure 8. Columns with light grey headers show the log(2) transformed regulation coefficient. Columns with dark grey headers show the corresponding p-value (*italics*). The cluster numbers correspond to the cluster numbers given in Supplemental Figure 8.

| Feature ID | Gene          | Annotation                                                         | NZ5521_s<br>tat | NZ5522_s<br>tat | NZ5523_s<br>tat | _IL594_s<br>tat | NZ5521_s<br>tat | NZ5522_s<br>tat | NZ5523_s<br>tat | _IL594_s<br>tat | Cluster |
|------------|---------------|--------------------------------------------------------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|---------|
| LLKF_0012  | <i>yabF</i>   | Hypothetical protein                                               | 1.50            | 1.01            | 0.20            | 2.49            | <i>0.037</i>    | <i>0.141</i>    | <i>0.813</i>    | <i>0.000</i>    | 1       |
| LLKF_0013  | <i>pth</i>    | Peptidyl-tRNA hydrolase                                            | 1.53            | 1.13            | 0.40            | 2.64            | <i>0.034</i>    | <i>0.091</i>    | <i>0.589</i>    | <i>0.000</i>    | 1       |
| LLKF_0014  | <i>mfd</i>    | Transcription-repair coupling factor                               | 0.82            | 0.59            | 0.53            | 3.37            | <i>0.155</i>    | <i>0.243</i>    | <i>0.407</i>    | <i>0.000</i>    | 1       |
| LLKF_0015  | <i>yacI</i>   | Hypothetical protein                                               | 0.12            | 0.16            | 0.11            | 1.98            | <i>0.606</i>    | <i>0.779</i>    | <i>0.874</i>    | <i>0.000</i>    | 1       |
| LLKF_0020  | <i>tilS</i>   | tRNA(Ile)-lysidine synthetase                                      | 1.76            | 1.47            | 0.60            | 1.88            | <i>0.020</i>    | <i>0.045</i>    | <i>0.400</i>    | <i>0.001</i>    | 1       |
| LLKF_0028  | <i>yafE</i>   | Acetyltransferase, GNAT family                                     | 1.19            | 0.69            | 0.18            | 2.05            | <i>0.065</i>    | <i>0.194</i>    | <i>0.716</i>    | <i>0.000</i>    | 1       |
| LLKF_0081  | <i>acpD</i>   | Acyl carrier protein phosphodiesterase                             | 0.16            | 0.37            | 0.19            | 2.77            | <i>0.812</i>    | <i>0.568</i>    | <i>0.827</i>    | <i>0.000</i>    | 1       |
| LLKF_0087  | <i>ybcG</i>   | Hypothetical protein, UPF0133 family                               | 2.06            | 1.88            | 0.54            | 2.00            | <i>0.008</i>    | <i>0.012</i>    | <i>0.346</i>    | <i>0.000</i>    | 1       |
| LLKF_0110  | <i>pmrB</i>   | Multidrug resistance efflux pump, MF superfamily                   | 2.96            | 2.89            | 1.04            | 2.55            | <i>0.004</i>    | <i>0.003</i>    | <i>0.112</i>    | <i>0.001</i>    | 1       |
| LLKF_0111  | <i>ybdA</i>   | Transcriptional regulator, TetR family                             | 3.33            | 3.07            | 0.01            | 3.07            | <i>0.001</i>    | <i>0.002</i>    | <i>0.876</i>    | <i>0.000</i>    | 1       |
| LLKF_0128  | <i>ybeF-C</i> | Collagen adhesion protein, LPXTG-anchored, C-terminus (pseudogene) | 0.72            | 0.66            | 0.49            | 2.84            | <i>0.384</i>    | <i>0.372</i>    | <i>0.558</i>    | <i>0.000</i>    | 1       |
| LLKF_0149  | <i>ybfB</i>   | DNA/RNA non-specific endonuclease                                  | 2.31            | 2.19            | 0.38            | 2.76            | <i>0.018</i>    | <i>0.022</i>    | <i>0.664</i>    | <i>0.000</i>    | 1       |
| LLKF_0150  | <i>ybfC</i>   | Hypothetical protein                                               | 3.50            | 2.81            | -0.02           | 1.21            | <i>0.000</i>    | <i>0.000</i>    | <i>0.974</i>    | <i>0.001</i>    | 1       |
| LLKF_0174  | <i>ybiB</i>   | 5'-Nucleotidase                                                    | 0.36            | 0.55            | 1.03            | 2.75            | <i>0.470</i>    | <i>0.256</i>    | <i>0.040</i>    | <i>0.000</i>    | 1       |
| LLKF_0175  | <i>ybiC</i>   | Hypothetical protein                                               | 0.12            | 0.17            | 0.35            | 2.46            | <i>0.507</i>    | <i>0.334</i>    | <i>0.569</i>    | <i>0.000</i>    | 1       |
| LLKF_0176  | <i>ybiD</i>   | Radical SAM family enzyme                                          | 0.32            | 0.27            | -0.03           | 1.95            | <i>0.581</i>    | <i>0.605</i>    | <i>0.909</i>    | <i>0.000</i>    | 1       |
| LLKF_0181  | <i>ybiK</i>   | Hypothetical protein                                               | 1.89            | 2.43            | 0.77            | 1.61            | <i>0.007</i>    | <i>0.002</i>    | <i>0.130</i>    | <i>0.001</i>    | 1       |
| LLKF_0226  | <i>ycdB</i>   | Hypothetical protein                                               | 0.55            | 0.62            | 0.48            | 2.26            | <i>0.245</i>    | <i>0.250</i>    | <i>0.346</i>    | <i>0.000</i>    | 1       |
| LLKF_0234  | <i>rpsU</i>   | SSU ribosomal protein S21P                                         | 2.82            | 2.62            | 0.69            | 2.83            | <i>0.001</i>    | <i>0.001</i>    | <i>0.138</i>    | <i>0.000</i>    | 1       |
| LLKF_0241  | <i>yceE</i>   | Hydrolase, HAD superfamily                                         | 2.61            | 2.15            | 0.59            | 3.12            | <i>0.015</i>    | <i>0.033</i>    | <i>0.556</i>    | <i>0.000</i>    | 1       |
| LLKF_0270  | <i>nrdD</i>   | Anaerobic ribonucleoside-triphosphate reductase                    | 2.34            | 1.52            | 0.16            | 1.11            | <i>0.001</i>    | <i>0.007</i>    | <i>0.773</i>    | <i>0.002</i>    | 1       |
| LLKF_0347  | <i>ycjH</i>   | Hypothetical protein                                               | 0.06            | 0.24            | -0.02           | 2.48            | <i>0.244</i>    | <i>0.627</i>    | <i>0.976</i>    | <i>0.000</i>    | 1       |
| LLKF_0349  | <i>phnC</i>   | Phosphonates ABC transporter ATP-binding protein PhnC              | 0.83            | 0.54            | 0.47            | 1.86            | <i>0.127</i>    | <i>0.377</i>    | <i>0.395</i>    | <i>0.000</i>    | 1       |

| Feature ID | Gene          | Annotation                                                                                      | NZ5521_s<br>tat | NZ5522_s<br>tat | NZ5523_s<br>tat | _IL594_s<br>tat | NZ5521_s<br>tat | NZ5522_s<br>tat | NZ5523_s<br>tat | IL594_s<br>tat | Clust<br>er |
|------------|---------------|-------------------------------------------------------------------------------------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|----------------|-------------|
| LLKF_0391  | <i>pmg</i>    | Phosphoglycerate mutase                                                                         | 0.97            | 1.03            | 0.42            | 1.97            | 0.122           | 0.122           | 0.506           | 0.001          | 1           |
| LLKF_0438  | <i>pepA-C</i> | Glutamyl aminopeptidase, C-terminal fragment (pseudogene)                                       | 1.51            | 1.41            | 0.58            | 2.02            | 0.024           | 0.028           | 0.307           | 0.000          | 1           |
| LLKF_0484  | <i>yeeC</i>   | Hypothetical protein                                                                            | 1.77            | 0.91            | 0.89            | 3.06            | 0.019           | 0.186           | 0.142           | 0.000          | 1           |
| LLKF_0506  | <i>hslA</i>   | DNA-binding protein HU, histone-like                                                            | 1.11            | 1.40            | 0.08            | 2.34            | 0.033           | 0.017           | 0.781           | 0.000          | 1           |
| LLKF_0534  | <i>yffA</i>   | Hypothetical protein                                                                            | 2.35            | 2.60            | 0.09            | 1.88            | 0.003           | 0.002           | 0.873           | 0.000          | 1           |
| LLKF_0535  | <i>clpE</i>   | ATP-dependent endopeptidase Clp, ATP-binding subunit ClpE                                       | 2.31            | 2.49            | -0.42           | 1.95            | 0.003           | 0.002           | 0.465           | 0.000          | 1           |
| LLKF_0536  | <i>yffB</i>   | Transcriptional regulator, Rrf2 family                                                          | 1.21            | 1.70            | 0.19            | 2.87            | 0.165           | 0.079           | 0.872           | 0.000          | 1           |
| LLKF_0549  | <i>yfgH</i>   | Hydrolase, HAD superfamily                                                                      | 2.74            | 2.48            | 0.87            | 1.95            | 0.001           | 0.001           | 0.077           | 0.000          | 1           |
| LLKF_0580  | <i>yffB</i>   | Hypothetical protein                                                                            | 0.67            | 0.70            | 0.46            | 2.33            | 0.332           | 0.313           | 0.503           | 0.000          | 1           |
| LLKF_0634  | <i>enoB</i>   | Enolase (phosphopyruvate hydratase)                                                             | 2.74            | 3.11            | 1.03            | 2.41            | 0.007           | 0.004           | 0.109           | 0.000          | 1           |
| LLKF_0646  | <i>gltA</i>   | Citrate synthase                                                                                | 0.44            | 0.08            | 0.18            | 2.26            | 0.430           | 0.581           | 0.737           | 0.000          | 1           |
| LLKF_0647  | <i>citB</i>   | Aconitate hydratase                                                                             | 0.06            | 0.18            | 0.23            | 2.72            | 0.609           | 0.737           | 0.726           | 0.000          | 1           |
| LLKF_0706  | <i>ygil</i>   | DNase, TatD family                                                                              | 1.56            | 1.48            | 0.48            | 2.30            | 0.028           | 0.026           | 0.429           | 0.000          | 1           |
| LLKF_0707  | <i>ygil</i>   | DNA topology modulation protein                                                                 | 1.42            | 1.23            | 0.32            | 2.61            | 0.046           | 0.085           | 0.680           | 0.000          | 1           |
| LLKF_0708  | <i>ygik</i>   | Ribonuclease M5                                                                                 | 0.79            | 0.68            | 0.03            | 2.39            | 0.149           | 0.214           | 0.968           | 0.000          | 1           |
| LLKF_0750  | <i>menX</i>   | Menaquinone biosynthesis related protein                                                        | 1.28            | 1.60            | -0.43           | 2.08            | 0.025           | 0.012           | 0.412           | 0.000          | 1           |
| LLKF_0751  | <i>menD</i>   | 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase/2-oxoglutarate decarboxylase | 1.21            | 1.43            | -0.54           | 2.01            | 0.048           | 0.022           | 0.284           | 0.000          | 1           |
| LLKF_0752  | <i>menF</i>   | Isochorismate synthase                                                                          | 1.94            | 1.68            | 0.17            | 2.19            | 0.009           | 0.017           | 0.790           | 0.000          | 1           |
| LLKF_0780  | <i>yhhB</i>   | Hypothetical protein, extracellular, LPXTG-anchored                                             | 0.76            | 0.85            | -0.08           | 2.95            | 0.315           | 0.269           | 0.940           | 0.000          | 1           |
| LLKF_0781  | <i>lrgB</i>   | Murein hydrolase export regulator                                                               | 1.31            | 1.56            | 0.62            | 1.77            | 0.077           | 0.030           | 0.436           | 0.001          | 1           |
| LLKF_0782  | <i>lrgA</i>   | Murein hydrolase exporter                                                                       | 3.03            | 2.41            | 1.50            | 2.56            | 0.001           | 0.002           | 0.010           | 0.000          | 1           |
| LLKF_0789  | <i>manA</i>   | Mannose-6-phosphate isomerase                                                                   | 2.43            | 2.10            | 0.14            | 1.98            | 0.002           | 0.003           | 0.744           | 0.000          | 1           |
| LLKF_0792  | <i>acpP</i>   | Acyl carrier protein                                                                            | 2.42            | 1.63            | 0.26            | 1.57            | 0.002           | 0.012           | 0.624           | 0.000          | 1           |
| LLKF_0834  | <i>leuS</i>   | Leucyl-tRNA synthetase                                                                          | 1.06            | 0.91            | 0.24            | 1.51            | 0.044           | 0.076           | 0.682           | 0.001          | 1           |
| LLKF_0844  | <i>copR</i>   | Copper transport repressor, CopY/TcrY family                                                    | 2.56            | 2.70            | 0.44            | 0.70            | 0.001           | 0.001           | 0.391           | 0.034          | 1           |
| LLKF_0845  | <i>copZ</i>   | Copper chaperone CopZ                                                                           | 2.84            | 3.02            | 0.44            | 1.07            | 0.001           | 0.000           | 0.359           | 0.004          | 1           |
| LLKF_0858  | <i>yigC</i>   | Arsenate reductase family protein                                                               | 0.62            | 0.03            | 0.24            | 2.72            | 0.226           | 0.674           | 0.707           | 0.000          | 1           |
| LLKF_0877  | <i>ispA</i>   | Dimethylallyltransferase/geranyltransferase                                                     | 1.08            | 1.33            | 0.23            | 1.51            | 0.049           | 0.029           | 0.663           | 0.001          | 1           |
| LLKF_0878  | <i>rrmJ</i>   | rRNA methylase                                                                                  | 0.68            | 0.92            | 0.04            | 1.62            | 0.192           | 0.092           | 0.900           | 0.001          | 1           |
| LLKF_0920  | <i>ppiB</i>   | Peptidyl-prolyl cis-trans isomerase                                                             | 0.58            | 0.74            | 0.24            | 1.49            | 0.212           | 0.130           | 0.637           | 0.001          | 1           |
| LLKF_0933  | <i>gyrB</i>   | DNA gyrase, subunit B                                                                           | 0.37            | 0.11            | 0.59            | 1.62            | 0.412           | 0.588           | 0.238           | 0.000          | 1           |
| LLKF_0937  | <i>yjdC</i>   | Transcriptional regulator, MarR family                                                          | 0.80            | 0.98            | -0.06           | 2.39            | 0.123           | 0.068           | 0.793           | 0.000          | 1           |
| LLKF_0938  | <i>yjdE</i>   | Multidrug resistance protein B, MF superfamily                                                  | 1.11            | 1.00            | -0.13           | 2.26            | 0.048           | 0.059           | 0.823           | 0.000          | 1           |
| LLKF_0939  | <i>yjdF</i>   | Hypothetical protein                                                                            | 0.96            | 1.16            | 0.38            | 1.98            | 0.141           | 0.085           | 0.604           | 0.001          | 1           |
| LLKF_0982  | <i>grpE</i>   | Molecular chaperone GrpE                                                                        | 3.19            | 3.04            | 0.61            | 2.53            | 0.006           | 0.008           | 0.519           | 0.001          | 1           |
| LLKF_1089  | <i>rex</i>    | Redox-sensing transcriptional repressor                                                         | 1.21            | 1.13            | -1.25           | 2.18            | 0.039           | 0.072           | 0.020           | 0.000          | 1           |
| LLKF_1109  | <i>rpmA</i>   | LSU ribosomal protein L27P                                                                      | 1.54            | 1.10            | 0.32            | 2.30            | 0.008           | 0.034           | 0.516           | 0.000          | 1           |
| LLKF_1122  | <i>glyQ</i>   | Glycyl-tRNA synthetase, alpha chain                                                             | 1.55            | 1.36            | 0.07            | 2.73            | 0.011           | 0.017           | 0.713           | 0.000          | 1           |
| LLKF_1123  | <i>glyS</i>   | Glycyl-tRNA synthetase, beta chain                                                              | 1.07            | 1.15            | -0.17           | 2.29            | 0.062           | 0.058           | 0.781           | 0.001          | 1           |

| Feature ID | Gene          | Annotation                                                | NZ5521_s<br>tat | NZ5522_s<br>tat | NZ5523_s<br>tat | _IL594_s<br>tat | NZ5521_s<br>tat | NZ5522_s<br>tat | NZ5523_s<br>tat | IL594_s<br>tat | Clust<br>er |
|------------|---------------|-----------------------------------------------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|----------------|-------------|
| LLKF_1124  | <i>ylaC</i>   | Hypothetical protein                                      | 1.13            | 1.31            | 0.31            | 2.50            | 0.098           | 0.045           | 0.658           | 0.000          | 1           |
| LLKF_1126  | <i>nadD2</i>  | Nicotinate-nucleotide adenylyltransferase                 | 0.10            | -0.06           | 0.20            | 1.60            | 0.628           | 0.885           | 0.724           | 0.000          | 1           |
| LLKF_1138  | <i>gyrA</i>   | DNA gyrase, subunit A                                     | 0.67            | 0.51            | 0.20            | 1.63            | 0.176           | 0.329           | 0.740           | 0.001          | 1           |
| LLKF_1139  | <i>apbE</i>   | Iron-sulfur cluster assembly/repair protein ApbE          | 0.21            | 0.33            | 0.28            | 3.01            | 0.550           | 0.534           | 0.651           | 0.000          | 1           |
| LLKF_1140  | <i>srtA-N</i> | Sortase, N-terminal fragment (pseudogene)                 | 1.73            | 1.57            | 0.53            | 2.43            | 0.032           | 0.045           | 0.470           | 0.000          | 1           |
| LLKF_1141  | <i>ylcF-N</i> | Hypothetical protein, N-terminal fragment (pseudogene)    | 3.20            | 2.80            | 0.55            | 3.29            | 0.010           | 0.018           | 0.629           | 0.001          | 1           |
| LLKF_1142  | <i>ylcF-C</i> | Hypothetical protein, C-terminal fragment (pseudogene)    | 2.88            | 2.92            | 0.49            | 2.80            | 0.010           | 0.010           | 0.627           | 0.001          | 1           |
| LLKF_1150  | <i>frdC</i>   | Fumarate reductase, flavoprotein subunit                  | 1.09            | 0.78            | 0.42            | 2.38            | 0.110           | 0.249           | 0.568           | 0.000          | 1           |
| LLKF_1159  | <i>tpiA</i>   | Triosephosphate isomerase                                 | 2.28            | 2.85            | 0.55            | 2.80            | 0.004           | 0.002           | 0.335           | 0.000          | 1           |
| LLKF_1162  | <i>lbrA</i>   | Co-activator of prophage gene expression LbrA             | 0.49            | 0.43            | 0.91            | 1.82            | 0.389           | 0.431           | 0.077           | 0.000          | 1           |
| LLKF_1163  | <i>lbrB</i>   | Co-activator of prophage gene expression LbrB             | 0.19            | 0.06            | 0.46            | 1.69            | 0.689           | 0.742           | 0.341           | 0.000          | 1           |
| LLKF_1165  | <i>ylfD</i>   | Peptidoglycan hydrolase, GH25 muramidase family           | 2.00            | 2.36            | 0.56            | 2.57            | 0.009           | 0.005           | 0.425           | 0.000          | 1           |
| LLKF_1188  | <i>murB</i>   | UDP-N-acetylenolpyruvoylglucosamine reductase             | 2.14            | 1.80            | 0.60            | 2.24            | 0.004           | 0.009           | 0.291           | 0.000          | 1           |
| LLKF_1208  | <i>als</i>    | Alpha-acetolactate synthase                               | 0.42            | 0.70            | -0.17           | 1.92            | 0.325           | 0.225           | 0.613           | 0.000          | 1           |
| LLKF_1260  | <i>leuA</i>   | 2-isopropylmalate synthase                                | 1.74            | 0.82            | 1.71            | 3.06            | 0.021           | 0.228           | 0.024           | 0.000          | 1           |
| LLKF_1261  | <i>leuB</i>   | 3-isopropylmalate dehydrogenase                           | 1.47            | 0.80            | 1.77            | 3.28            | 0.085           | 0.307           | 0.061           | 0.000          | 1           |
| LLKF_1263  | <i>leuC</i>   | 3-isopropylmalate dehydratase, large subunit              | 1.77            | 1.12            | 1.76            | 3.15            | 0.103           | 0.229           | 0.043           | 0.000          | 1           |
| LLKF_1264  | <i>leuD</i>   | 3-isopropylmalate dehydratase, small subunit              | 1.59            | 0.18            | 2.16            | 3.60            | 0.111           | 0.792           | 0.041           | 0.000          | 1           |
| LLKF_1266  | <i>ilvD</i>   | Dihydroxy-acid dehydratase                                | 1.36            | 0.25            | 1.35            | 3.08            | 0.099           | 0.743           | 0.100           | 0.000          | 1           |
| LLKF_1351  | <i>gltD</i>   | Glutamate synthase [NADPH], small chain                   | 0.50            | -0.33           | 0.79            | 1.79            | 0.360           | 0.536           | 0.148           | 0.001          | 1           |
| LLKF_1363  | <i>rdrB</i>   | Transcriptional regulator, DeoR family                    | 1.59            | 1.46            | 0.14            | 2.69            | 0.220           | 0.100           | 0.862           | 0.000          | 1           |
| LLKF_1422  | <i>ldhL</i>   | L-lactate dehydrogenase                                   | 1.13            | 1.27            | 0.72            | 3.26            | 0.024           | 0.015           | 0.126           | 0.000          | 1           |
| LLKF_1426  | <i>nagA</i>   | N-acetylglucosamine-6-phosphate deacetylase               | 2.03            | 1.54            | 0.97            | 2.07            | 0.008           | 0.025           | 0.119           | 0.001          | 1           |
| LLKF_1455  | <i>yoaB</i>   | Calcium-transporting ATPase                               | 0.24            | -0.01           | 0.56            | 2.03            | 0.658           | 0.449           | 0.287           | 0.000          | 1           |
| LLKF_1456  | <i>yoaD</i>   | Hypothetical protein                                      | 1.84            | 1.43            | 0.39            | 2.22            | 0.018           | 0.039           | 0.555           | 0.000          | 1           |
| LLKF_1630  | <i>xylR</i>   | Transcriptional regulator, AraC family                    | 3.01            | 2.35            | 0.35            | 2.74            | 0.001           | 0.004           | 0.593           | 0.000          | 1           |
| LLKF_1642  | <i>purN</i>   | Phosphoribosylglycinamide formyltransferase               | 1.74            | 1.27            | 0.44            | 1.78            | 0.004           | 0.014           | 0.312           | 0.000          | 1           |
| LLKF_1652  | <i>purQ</i>   | Phosphoribosylformylglycinamide synthase I                | 0.31            | -0.02           | 0.64            | 1.44            | 0.522           | 0.490           | 0.228           | 0.001          | 1           |
| LLKF_1664  | <i>ypiE-N</i> | Hypothetical protein , N-terminal fragment (pseudogene)   | 0.64            | 0.69            | -0.11           | 1.91            | 0.318           | 0.283           | 0.904           | 0.001          | 1           |
| LLKF_1668  | <i>ypiJ-N</i> | Hypothetical protein , N-terminal fragment (pseudogene)   | 1.11            | 0.53            | 0.64            | 2.43            | 0.142           | 0.571           | 0.429           | 0.001          | 1           |
| LLKF_1669  | <i>ypiK</i>   | Hypothetical protein                                      | 0.79            | 0.01            | 0.00            | 2.50            | 0.281           | 0.989           | 0.998           | 0.000          | 1           |
| LLKF_1670  | <i>ypiL</i>   | Hypothetical protein, extracellular, C-terminal TM anchor | 1.21            | 0.67            | 0.21            | 2.38            | 0.175           | 0.366           | 0.720           | 0.001          | 1           |
| LLKF_1742  | <i>amtB</i>   | Ammonium/methylammonium transporter                       | 0.40            | 0.36            | -0.03           | 2.02            | 0.504           | 0.550           | 0.978           | 0.000          | 1           |
| LLKF_1758  | <i>rarA</i>   | Transcriptional regulator, ArsR family                    | 3.56            | 3.02            | 1.55            | 2.39            | 0.002           | 0.003           | 0.038           | 0.000          | 1           |
| LLKF_1759  | <i>yqel</i>   | Cobalt-zinc-cadmium transporter                           | 3.48            | 3.09            | 1.62            | 2.17            | 0.001           | 0.001           | 0.016           | 0.000          | 1           |
| LLKF_1778  | <i>yqgF</i>   | Hypothetical protein                                      | 0.08            | 0.49            | -0.17           | 2.20            | 0.606           | 0.371           | 0.784           | 0.000          | 1           |
| LLKF_1811  | <i>holA</i>   | DNA polymerase III, delta subunit                         | 1.64            | 1.35            | 0.46            | 2.94            | 0.016           | 0.030           | 0.407           | 0.000          | 1           |
| LLKF_1812  | <i>yraD</i>   | Hypothetical protein                                      | 1.24            | 1.24            | 0.47            | 2.52            | 0.035           | 0.037           | 0.396           | 0.000          | 1           |
| LLKF_1813  | <i>ftsK</i>   | DNA translocase FtsK                                      | 1.62            | 1.54            | 0.58            | 2.28            | 0.030           | 0.032           | 0.346           | 0.000          | 1           |
| LLKF_1886  | <i>phoU</i>   | Phosphate transport system regulator                      | 2.41            | 2.59            | 0.41            | 2.72            | 0.008           | 0.006           | 0.595           | 0.000          | 1           |

| Feature ID | Gene         | Annotation                                                                            | NZ5521_s<br>tat | NZ5522_s<br>tat | NZ5523_s<br>tat | _IL594_s<br>tat | NZ5521_s<br>tat | NZ5522_s<br>tat | NZ5523_s<br>tat | IL594_s<br>tat | Clust<br>er |
|------------|--------------|---------------------------------------------------------------------------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|----------------|-------------|
| LLKF_1887  | <i>pstA</i>  | Phosphate ABC transporter, ATP-binding protein                                        | 1.92            | 1.88            | 0.14            | 2.27            | 0.005           | 0.006           | 0.832           | 0.000          | 1           |
| LLKF_1888  | <i>pstB</i>  | Phosphate ABC transporter, ATP-binding protein                                        | 2.18            | 2.16            | 0.18            | 2.42            | 0.003           | 0.004           | 0.733           | 0.000          | 1           |
| LLKF_1889  | <i>pstC</i>  | Phosphate ABC transporter, permease protein                                           | 2.05            | 2.49            | 0.37            | 2.08            | 0.003           | 0.001           | 0.472           | 0.000          | 1           |
| LLKF_1890  | <i>pstD</i>  | Phosphate ABC transporter, permease protein                                           | 2.59            | 2.75            | 0.40            | 1.89            | 0.001           | 0.001           | 0.438           | 0.000          | 1           |
| LLKF_1891  | <i>pstE</i>  | Phosphate ABC transporter, substrate-binding protein                                  | 2.72            | 2.62            | 0.53            | 2.31            | 0.001           | 0.002           | 0.337           | 0.000          | 1           |
| LLKF_1987  | <i>pflA</i>  | Pyruvate formate-lyase activating enzyme                                              | 3.74            | 3.02            | 0.66            | 2.45            | 0.001           | 0.005           | 0.315           | 0.000          | 1           |
| LLKF_2011  | <i>uvrA</i>  | Excinuclease ABC, subunit A                                                           | 1.69            | 2.22            | -0.02           | 1.95            | 0.019           | 0.006           | 0.949           | 0.001          | 1           |
| LLKF_2012  | <i>ysiE</i>  | Hypothetical protein                                                                  | 2.23            | 2.62            | 0.41            | 2.37            | 0.008           | 0.004           | 0.574           | 0.000          | 1           |
| LLKF_2014  | <i>ysiG</i>  | GIY-YIG nuclease superfamily protein                                                  | 0.08            | 0.22            | 0.28            | 1.82            | 0.462           | 0.426           | 0.610           | 0.000          | 1           |
| LLKF_2026  | <i>corC</i>  | Magnesium and cobalt efflux protein                                                   | 1.63            | 1.75            | 1.38            | 2.06            | 0.010           | 0.009           | 0.012           | 0.000          | 1           |
| LLKF_2035  | <i>rpml</i>  | LSU ribosomal protein L35P                                                            | 3.64            | 2.88            | 0.43            | 2.23            | 0.001           | 0.003           | 0.548           | 0.000          | 1           |
| LLKF_2036  | <i>infC</i>  | Translation Initiation Factor 3 (IF-3)                                                | 1.52            | 1.14            | 0.80            | 2.16            | 0.016           | 0.047           | 0.121           | 0.000          | 1           |
| LLKF_2042  | <i>ytbD</i>  | Hypothetical protein                                                                  | 3.16            | 2.73            | 0.53            | 1.18            | 0.001           | 0.002           | 0.353           | 0.005          | 1           |
| LLKF_2098  | <i>ythA</i>  | Stress-responsive transcriptional regulator, PspC family                              | 2.07            | 1.79            | -0.31           | 1.88            | 0.003           | 0.007           | 0.566           | 0.000          | 1           |
| LLKF_2099  | <i>ythB</i>  | Stress-responsive transcriptional regulator, PspC family                              | 1.91            | 1.81            | -0.01           | 1.91            | 0.015           | 0.017           | 0.920           | 0.000          | 1           |
| LLKF_2100  | <i>ythC</i>  | Hypothetical protein                                                                  | 2.33            | 2.02            | 0.00            | 2.26            | 0.003           | 0.005           | 0.924           | 0.000          | 1           |
| LLKF_2102  | <i>fbaA</i>  | Fructose-bisphosphate aldolase                                                        | 0.94            | 1.21            | 1.41            | 1.81            | 0.138           | 0.058           | 0.031           | 0.001          | 1           |
| LLKF_2104  | <i>thrS</i>  | Threonyl-tRNA synthetase                                                              | 1.34            | 1.02            | -0.14           | 1.55            | 0.023           | 0.070           | 0.780           | 0.001          | 1           |
| LLKF_2105  | <i>ytjA</i>  | Hypothetical protein                                                                  | 4.08            | 3.25            | -0.35           | 2.13            | 0.000           | 0.001           | 0.550           | 0.000          | 1           |
| LLKF_2107  | <i>ytjD</i>  | Nitroreductase family protein                                                         | 2.92            | 2.89            | 0.48            | 0.03            | 0.001           | 0.001           | 0.355           | 0.634          | 1           |
| LLKF_2123  | <i>pheT</i>  | Phenylalanyl-tRNA synthetase, beta chain                                              | 4.27            | 3.71            | 0.23            | 0.93            | 0.000           | 0.000           | 0.697           | 0.030          | 1           |
| LLKF_2126  | <i>yucF</i>  | Transcriptional regulator, PadR family                                                | 2.04            | 1.53            | 0.67            | 1.68            | 0.005           | 0.017           | 0.211           | 0.001          | 1           |
| LLKF_2129  | <i>purA</i>  | Adenylosuccinate synthetase                                                           | 3.47            | 2.04            | 0.40            | 2.01            | 0.001           | 0.006           | 0.506           | 0.000          | 1           |
| LLKF_2155  | <i>yueD</i>  | Transcriptional regulator, XRE family                                                 | 0.94            | 0.80            | 0.00            | 1.63            | 0.082           | 0.128           | 0.891           | 0.000          | 1           |
| LLKF_2178  | <i>yuhC</i>  | Hypothetical protein                                                                  | 1.43            | 1.37            | 0.54            | 2.20            | 0.041           | 0.062           | 0.307           | 0.000          | 1           |
| LLKF_2180  | <i>cutC</i>  | Copper homeostasis protein                                                            | 1.36            | 0.95            | 0.14            | 1.65            | 0.037           | 0.105           | 0.829           | 0.001          | 1           |
| LLKF_2204  | <i>yujC</i>  | Hypothetical protein, extracellular                                                   | 3.30            | 2.90            | 0.07            | 2.95            | 0.002           | 0.003           | 0.943           | 0.000          | 1           |
| LLKF_2226  | <i>murC</i>  | UDP-N-acetylmuramate--alanine ligase                                                  | 1.43            | 1.68            | 0.76            | 1.81            | 0.017           | 0.010           | 0.183           | 0.000          | 1           |
| LLKF_2389  | <i>ywbA</i>  | Methyltransferase                                                                     | 0.14            | 0.31            | -0.18           | 2.82            | 0.570           | 0.372           | 0.764           | 0.000          | 1           |
| LLKF_2398  | <i>adhE</i>  | Bifunctional protein: Alcohol dehydrogenase/ Acetaldehyde dehydrogenase [acetylating] | 2.98            | 2.56            | 0.31            | 3.33            | 0.002           | 0.003           | 0.645           | 0.000          | 1           |
| LLKF_2416  | <i>yweD</i>  | Hypothetical protein                                                                  | 2.16            | 2.45            | 0.02            | 2.95            | 0.028           | 0.017           | 0.941           | 0.001          | 1           |
| LLKF_2418  | <i>yweF</i>  | Hypothetical protein                                                                  | 2.30            | 2.13            | 0.53            | 2.29            | 0.014           | 0.032           | 0.521           | 0.001          | 1           |
| LLKF_2434  | <i>rpsR</i>  | SSU ribosomal protein S18P                                                            | 2.42            | 1.90            | 0.18            | 1.90            | 0.002           | 0.008           | 0.770           | 0.000          | 1           |
| LLKF_2436  | <i>rpsF</i>  | SSU ribosomal protein S6P                                                             | 1.29            | 0.60            | 0.35            | 1.47            | 0.028           | 0.260           | 0.532           | 0.001          | 1           |
| LLKF_2449  | <i>pp406</i> | Phage protein                                                                         | 0.88            | 0.72            | 0.55            | 2.95            | 0.158           | 0.182           | 0.345           | 0.000          | 1           |
| LLKF_2482  | <i>mutS</i>  | DNA mismatch repair protein MutS                                                      | 1.56            | 1.54            | 0.50            | 2.70            | 0.042           | 0.048           | 0.526           | 0.000          | 1           |
| LLKF_2501  | <i>rcfB</i>  | Transcription regulator, Crp family                                                   | 0.20            | 0.64            | 2.93            | 2.42            | 0.705           | 0.337           | 0.001           | 0.000          | 1           |
| LLKF_2517  | <i>yxdD</i>  | Transcriptional regulator, TetR family                                                | 2.59            | 2.10            | 0.78            | 3.15            | 0.011           | 0.027           | 0.332           | 0.000          | 1           |
| LLKF_0052  | <i>cysD</i>  | O-acetyl-L-homoserine sulphydrolase / O-acetyl-L-serine sulphydrolase                 | -1.84           | -2.15           | -1.29           | -2.28           | 0.021           | 0.009           | 0.026           | 0.000          | 2           |

| Feature ID | Gene          | Annotation                                                                       | NZ5521_s<br>tat | NZ5522_s<br>tat | NZ5523_s<br>tat | _IL594_s<br>tat | NZ5521_s<br>tat | NZ5522_s<br>tat | NZ5523_s<br>tat | _IL594_s<br>tat | Clust<br>er |
|------------|---------------|----------------------------------------------------------------------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-------------|
| LLKF_0073  | <i>relA</i>   | GTP pyrophosphokinase / Guanosine-3',5'-bis(Diphosphate) 3'-pyrophosphohydrolase | -1.83           | -1.79           | -0.89           | -2.50           | 0.012           | 0.023           | 0.119           | 0.000           | 2           |
| LLKF_0079  | <i>ybbE</i>   | 1-Acyl-sn-glycerol-3-phosphate acyltransferase                                   | -0.39           | -0.81           | -0.43           | -1.92           | 0.542           | 0.171           | 0.454           | 0.000           | 2           |
| LLKF_0083  | <i>aroF</i>   | 3-deoxy-7-phosphoheptulonate synthase                                            | -2.08           | -2.33           | -1.12           | -2.69           | 0.027           | 0.018           | 0.162           | 0.001           | 2           |
| LLKF_0088  | <i>ybcH</i>   | Alpha/beta hydrolase                                                             | -1.17           | -1.05           | -0.82           | -2.54           | 0.128           | 0.096           | 0.174           | 0.000           | 2           |
| LLKF_0116  | <i>ybdE</i>   | Aldo/keto reductase                                                              | -1.46           | -1.36           | -0.55           | -1.98           | 0.034           | 0.038           | 0.333           | 0.001           | 2           |
| LLKF_0159  | <i>ybgE</i>   | Amidase                                                                          | -1.36           | -1.42           | -0.94           | -1.65           | 0.022           | 0.017           | 0.082           | 0.001           | 2           |
| LLKF_0163  | <i>ybhB</i>   | Intramembrane serine protease, rhomboid family                                   | -0.49           | -0.64           | -0.56           | -1.46           | 0.470           | 0.393           | 0.271           | 0.001           | 2           |
| LLKF_0164  | <i>ybhC</i>   | Hypothetical protein                                                             | -1.63           | -1.63           | -1.52           | -1.95           | 0.017           | 0.018           | 0.017           | 0.000           | 2           |
| LLKF_0166  | <i>ybhE</i>   | Hypothetical protein                                                             | -2.59           | -3.09           | -2.78           | -3.44           | 0.011           | 0.005           | 0.006           | 0.000           | 2           |
| LLKF_0168  |               | Hypothetical protein                                                             | -2.40           | -2.35           | -1.74           | -2.70           | 0.004           | 0.005           | 0.007           | 0.000           | 2           |
| LLKF_0169  |               | Hypothetical protein                                                             | -1.54           | -1.73           | -1.44           | -2.41           | 0.042           | 0.029           | 0.047           | 0.000           | 2           |
| LLKF_0170  | <i>bglS</i>   | 6-Phospho-beta-glucosidase                                                       | -2.24           | -2.33           | -1.72           | -3.60           | 0.012           | 0.008           | 0.023           | 0.000           | 2           |
| LLKF_0177  | <i>ybiE</i>   | Nitroreductase family protein                                                    | -1.15           | -1.54           | -0.70           | -2.41           | 0.055           | 0.024           | 0.202           | 0.000           | 2           |
| LLKF_0185  | <i>ybjJ</i>   | Dihydroxyacetone kinase family protein                                           | -0.90           | -1.10           | -0.26           | -3.08           | 0.164           | 0.086           | 0.701           | 0.000           | 2           |
| LLKF_0186  | <i>ybjK</i>   | General stress protein, Gls24 family                                             | -1.36           | -1.47           | -0.40           | -3.37           | 0.064           | 0.054           | 0.593           | 0.000           | 2           |
| LLKF_0249  | <i>pepD1A</i> | Dipeptidase PepD                                                                 | -1.41           | -1.58           | -0.87           | -2.07           | 0.121           | 0.046           | 0.157           | 0.001           | 2           |
| LLKF_0253  | <i>fbp1</i>   | Fructose-1,6-bisphosphatase                                                      | -1.42           | -1.35           | -1.24           | -2.82           | 0.032           | 0.086           | 0.048           | 0.000           | 2           |
| LLKF_0261  | <i>ycgC</i>   | Hypothetical protein                                                             | -1.25           | -1.03           | -0.60           | -1.61           | 0.041           | 0.121           | 0.242           | 0.001           | 2           |
| LLKF_0264  | <i>ycgF</i>   | Transcription activator                                                          | -2.56           | -1.99           | 0.35            | -2.52           | 0.006           | 0.018           | 0.668           | 0.000           | 2           |
| LLKF_0265  | <i>ycgG</i>   | Aldo/keto reductase                                                              | -2.34           | -1.83           | 0.14            | -2.65           | 0.006           | 0.028           | 0.766           | 0.000           | 2           |
| LLKF_0330  | <i>ychH</i>   | Tetrahydrodipicolinate N-acetyltransferase                                       | -1.38           | -1.55           | -0.52           | -1.68           | 0.031           | 0.022           | 0.367           | 0.001           | 2           |
| LLKF_0369  | <i>bioY</i>   | Biotin transporter                                                               | -0.59           | -0.79           | -0.41           | -1.90           | 0.303           | 0.160           | 0.511           | 0.001           | 2           |
| LLKF_0375  | <i>plpD</i>   | ABC transporter, substrate-binding protein, NLPA lipofamily                      | -3.25           | -3.32           | 0.35            | -1.78           | 0.002           | 0.001           | 0.570           | 0.001           | 2           |
| LLKF_0377  | <i>ydC</i>    | ABC transporter, permease protein                                                | -3.33           | -3.32           | 0.02            | -2.36           | 0.002           | 0.002           | 0.957           | 0.000           | 2           |
| LLKF_0378  | <i>cbiQ1</i>  | ABC-type cobalt transporter, permease protein CbiQ                               | -2.99           | -2.90           | 0.15            | -2.66           | 0.002           | 0.003           | 0.768           | 0.000           | 2           |
| LLKF_0389  | <i>yddC</i>   | Transcriptional regulator, MarR family                                           | -1.52           | -1.46           | -0.51           | -2.02           | 0.012           | 0.013           | 0.305           | 0.000           | 2           |
| LLKF_0390  | <i>yddD</i>   | Glyoxalase family protein                                                        | -1.46           | -1.14           | -0.78           | -2.39           | 0.033           | 0.065           | 0.199           | 0.000           | 2           |
| LLKF_0400  | <i>optB</i>   | Oligopeptide ABC transporter, permease protein                                   | -1.13           | -1.49           | 0.18            | -3.51           | 0.044           | 0.017           | 0.787           | 0.000           | 2           |
| LLKF_0401  | <i>optC</i>   | Oligopeptide ABC transporter, permease protein                                   | -0.95           | -1.28           | 0.50            | -3.40           | 0.116           | 0.035           | 0.366           | 0.000           | 2           |
| LLKF_0402  | <i>optD</i>   | Oligopeptide ABC transporter, ATP-binding protein                                | -1.47           | -1.68           | 0.65            | -2.77           | 0.015           | 0.009           | 0.210           | 0.000           | 2           |
| LLKF_0403  | <i>optF</i>   | Oligopeptide ABC transporter, ATP-binding protein                                | -1.29           | -1.60           | 0.57            | -3.24           | 0.081           | 0.034           | 0.353           | 0.000           | 2           |
| LLKF_0421  | <i>lysQ</i>   | Lysine-specific permease                                                         | -1.62           | -1.75           | -1.13           | -2.99           | 0.022           | 0.021           | 0.070           | 0.000           | 2           |
| LLKF_0436  | <i>tyrS</i>   | Tyrosyl-tRNA synthetase                                                          | -0.85           | -0.75           | 0.02            | -2.39           | 0.151           | 0.221           | 0.876           | 0.000           | 2           |
| LLKF_0440  |               | Hypothetical protein                                                             | -1.25           | -1.20           | -0.26           | -1.98           | 0.082           | 0.082           | 0.702           | 0.001           | 2           |
| LLKF_0441  | <i>trxH</i>   | Thioredoxin                                                                      | -1.44           | -1.56           | -0.50           | -1.72           | 0.021           | 0.016           | 0.375           | 0.001           | 2           |
| LLKF_0443  | <i>noxE</i>   | NADH oxidase, H2O-forming                                                        | -1.10           | -0.86           | -0.22           | -2.00           | 0.032           | 0.077           | 0.695           | 0.000           | 2           |
| LLKF_0463  | <i>yebE</i>   | Hypothetical protein                                                             | -1.68           | -1.63           | -0.53           | -2.60           | 0.005           | 0.006           | 0.241           | 0.000           | 2           |
| LLKF_0465  | <i>ptcB</i>   | PTS system, cellobiose-specific IIB component                                    | -3.54           | -3.17           | -1.35           | -2.07           | 0.001           | 0.001           | 0.031           | 0.001           | 2           |
| LLKF_0482  | <i>pgmB</i>   | Beta-phosphoglucomutase                                                          | -1.58           | -1.12           | -0.72           | -2.00           | 0.024           | 0.088           | 0.230           | 0.000           | 2           |

| Feature ID | Gene         | Annotation                                                                                | NZ5521_s<br>tat | NZ5522_s<br>tat | NZ5523_s<br>tat | _IL594_s<br>tat | NZ5521_s<br>tat | NZ5522_s<br>tat | NZ5523_s<br>tat | _IL594_s<br>tat | Clust<br>er |
|------------|--------------|-------------------------------------------------------------------------------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-------------|
| LLKF_0596  | <i>ptsK</i>  | Hpr(Ser) kinase                                                                           | -1.43           | -1.49           | -0.43           | -2.15           | 0.033           | 0.024           | 0.473           | 0.000           | 2           |
| LLKF_0598  | <i>ygaI</i>  | Hypothetical protein                                                                      | -2.17           | -1.50           | -0.06           | -2.04           | 0.003           | 0.012           | 0.936           | 0.000           | 2           |
| LLKF_0599  | <i>ygaJ</i>  | Hypothetical protein                                                                      | -2.29           | -1.62           | -0.03           | -1.85           | 0.006           | 0.045           | 0.891           | 0.000           | 2           |
| LLKF_0622  | <i>ygbE</i>  | Membrane protease protein family                                                          | -0.49           | -0.38           | -0.58           | -2.70           | 0.364           | 0.497           | 0.270           | 0.000           | 2           |
| LLKF_0640  | <i>pfl</i>   | Formate acetyltransferase                                                                 | -2.97           | -3.17           | -0.62           | -3.37           | 0.002           | 0.002           | 0.380           | 0.000           | 2           |
| LLKF_0650  | <i>yghB</i>  | Hypothetical protein                                                                      | -1.07           | -0.88           | -0.62           | -2.25           | 0.157           | 0.136           | 0.282           | 0.000           | 2           |
| LLKF_0715  | <i>glgC</i>  | Glucose-1-phosphate adenylyltransferase, catalytic subunit                                | -1.68           | -1.98           | -1.96           | -2.97           | 0.016           | 0.009           | 0.006           | 0.000           | 2           |
| LLKF_0716  | <i>glgD</i>  | Glucose-1-phosphate adenylyltransferase, regulatory subunit                               | -1.37           | -1.51           | -1.57           | -2.23           | 0.020           | 0.014           | 0.008           | 0.000           | 2           |
| LLKF_0719  | <i>apu</i>   | Glucan 1,4- $\beta$ -maltohydrolase                                                       | -2.57           | -1.94           | -0.93           | -1.86           | 0.001           | 0.005           | 0.070           | 0.000           | 2           |
| LLKF_0849  | <i>trmU</i>  | tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase                              | -0.29           | -0.82           | -0.06           | -2.96           | 0.484           | 0.125           | 0.897           | 0.000           | 2           |
| LLKF_0855  | <i>pepV</i>  | Dipeptidase                                                                               | -0.97           | -0.81           | 0.19            | -1.90           | 0.127           | 0.222           | 0.710           | 0.000           | 2           |
| LLKF_0860  | <i>choQ</i>  | Glycine betaine ABC transporter, ATP-binding protein                                      | -1.48           | -1.34           | -0.24           | -2.13           | 0.036           | 0.054           | 0.736           | 0.000           | 2           |
| LLKF_0900  | <i>yjaB</i>  | Universal stress protein family                                                           | -0.35           | -0.76           | -0.62           | -1.58           | 0.554           | 0.179           | 0.290           | 0.001           | 2           |
| LLKF_0985  | <i>yjiB</i>  | N-acyl-L-amino acid amidohydrolase                                                        | -0.62           | -1.17           | 0.63            | -2.45           | 0.318           | 0.063           | 0.248           | 0.000           | 2           |
| LLKF_1000  | <i>prfB</i>  | Peptide chain release factor 2 (RF-2)                                                     | -1.04           | -0.72           | -0.13           | -1.54           | 0.059           | 0.201           | 0.505           | 0.001           | 2           |
| LLKF_1014  | <i>corA3</i> | Mg2+ and Co2+ transporter, CorA family                                                    | -0.98           | -0.82           | 0.01            | -1.67           | 0.106           | 0.164           | 0.937           | 0.001           | 2           |
| LLKF_1131  | <i>ylbB</i>  | ABC transporter, permease protein                                                         | -1.90           | -1.71           | -1.10           | -2.24           | 0.019           | 0.024           | 0.091           | 0.000           | 2           |
| LLKF_1275  | <i>trmFO</i> | tRNA (uracil-5-)-methyltransferase Gid                                                    | -1.40           | -1.14           | -0.16           | -2.17           | 0.046           | 0.085           | 0.643           | 0.000           | 2           |
| LLKF_1338  | <i>ynaC</i>  | Multidrug/protein/lipid ABC transporter family, ATP-binding and permease protein          | -1.14           | -1.09           | -0.39           | -1.60           | 0.136           | 0.105           | 0.486           | 0.001           | 2           |
| LLKF_1354  | <i>bcaT</i>  | Branched-chain amino acid aminotransferase                                                | -1.65           | -2.26           | -0.53           | -2.16           | 0.028           | 0.005           | 0.372           | 0.000           | 2           |
| LLKF_1406  | <i>mtsC</i>  | Manganese ABC transporter, permease protein                                               | -1.10           | -1.15           | -0.22           | -2.92           | 0.069           | 0.058           | 0.735           | 0.000           | 2           |
| LLKF_1420  | <i>yngF</i>  | Nucleoside ABC transporter, permease protein                                              | -1.67           | -1.93           | -0.36           | -1.73           | 0.009           | 0.008           | 0.540           | 0.000           | 2           |
| LLKF_1421  | <i>yngG</i>  | Nucleoside ABC transporter, permease protein                                              | -1.56           | -1.81           | -0.30           | -2.17           | 0.011           | 0.009           | 0.570           | 0.000           | 2           |
| LLKF_1558  | <i>busAB</i> | Glycine betaine/carnitine/choline ABC transporter, permease and substrate-binding protein | -1.71           | -1.28           | 1.04            | -2.40           | 0.038           | 0.086           | 0.066           | 0.000           | 2           |
| LLKF_1559  | <i>busAA</i> | Glycine betaine/carnitine/choline ABC transporter, ATP-binding protein                    | -2.13           | -1.83           | 0.98            | -2.27           | 0.002           | 0.006           | 0.043           | 0.000           | 2           |
| LLKF_1572  | <i>trpG</i>  | Anthranilate synthase component II                                                        | -2.81           | -2.69           | -0.88           | -1.61           | 0.001           | 0.001           | 0.069           | 0.000           | 2           |
| LLKF_1573  | <i>trpE</i>  | Anthranilate synthase component I                                                         | -1.48           | -1.88           | -1.15           | -1.82           | 0.053           | 0.007           | 0.041           | 0.000           | 2           |
| LLKF_1575  | <i>ypaA</i>  | Hypothetical protein                                                                      | -0.47           | -0.52           | -0.77           | -2.69           | 0.322           | 0.288           | 0.123           | 0.000           | 2           |
| LLKF_1601  | <i>fruK</i>  | Fructokinase                                                                              | -1.39           | -1.65           | -1.07           | -2.12           | 0.042           | 0.017           | 0.071           | 0.000           | 2           |
| LLKF_1602  | <i>glcK</i>  | Glucokinase / transcription regulator. ROK family                                         | -1.84           | -1.93           | -1.42           | -2.00           | 0.028           | 0.029           | 0.032           | 0.001           | 2           |
| LLKF_1604  | <i>ypcB</i>  | Hypothetical protein                                                                      | -1.12           | -1.48           | -1.25           | -1.99           | 0.075           | 0.031           | 0.034           | 0.000           | 2           |
| LLKF_1606  | <i>dexB</i>  | Glucan 1,6- $\alpha$ -glucosidase                                                         | -0.94           | -1.09           | -1.52           | -2.23           | 0.237           | 0.129           | 0.039           | 0.001           | 2           |
| LLKF_1608  | <i>ypcG</i>  | Sugar ABC transporter, substrate-binding protein                                          | -2.62           | -2.87           | -1.77           | -4.61           | 0.016           | 0.014           | 0.053           | 0.000           | 2           |
| LLKF_1609  | <i>ypcH</i>  | Sugar ABC transporter, permease protein                                                   | -2.00           | -2.73           | -1.89           | -4.34           | 0.021           | 0.008           | 0.020           | 0.000           | 2           |
| LLKF_1610  | <i>ypdA</i>  | Sugar ABC transporter, permease protein                                                   | -1.80           | -1.77           | -1.64           | -3.93           | 0.124           | 0.113           | 0.029           | 0.000           | 2           |
| LLKF_1611  | <i>ypdB</i>  | Alpha-mannosidase                                                                         | -2.12           | -2.59           | -1.83           | -4.01           | 0.030           | 0.014           | 0.038           | 0.000           | 2           |
| LLKF_1612  | <i>ypdC</i>  | Hypothetical protein                                                                      | -2.82           | -2.40           | -1.67           | -3.15           | 0.017           | 0.026           | 0.058           | 0.001           | 2           |
| LLKF_1636  | <i>ypfF</i>  | Hydrolase, HAD superfamily                                                                | -1.95           | -2.06           | -1.40           | -1.99           | 0.022           | 0.007           | 0.033           | 0.001           | 2           |

| Feature ID | Gene             | Annotation                                                            | NZ5521_s<br>tat | NZ5522_s<br>tat | NZ5523_s<br>tat | _IL594_s<br>tat | NZ5521_s<br>tat | NZ5522_s<br>tat | NZ5523_s<br>tat | _IL594_s<br>tat | Clust<br>er |
|------------|------------------|-----------------------------------------------------------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-------------|
| LLKF_1671  | <i>ypjA</i>      | Zinc-binding alcohol dehydrogenase                                    | -1.66           | -1.49           | -0.95           | -1.67           | 0.014           | 0.018           | 0.110           | 0.001           | 2           |
| LLKF_1672  | <i>ypjB</i>      | Hypothetical protein                                                  | -1.47           | -0.93           | -0.48           | -1.96           | 0.018           | 0.046           | 0.271           | 0.000           | 2           |
| LLKF_1674  | <i>pydA</i>      | Dihydroorotate dehydrogenase                                          | -1.11           | -0.91           | -0.66           | -2.57           | 0.123           | 0.221           | 0.288           | 0.000           | 2           |
| LLKF_1748  | <i>yqeB</i>      | Hypothetical protein                                                  | -2.12           | -1.55           | -0.38           | -2.42           | 0.005           | 0.019           | 0.533           | 0.000           | 2           |
| LLKF_1773  |                  | Hypothetical protein                                                  | -1.54           | -1.39           | -0.30           | -2.23           | 0.012           | 0.018           | 0.611           | 0.000           | 2           |
| LLKF_1774  | <i>yqgC</i>      | Phosphohydrolase, MutT/nudix family protein                           | -0.95           | -0.49           | -0.76           | -1.64           | 0.050           | 0.277           | 0.099           | 0.000           | 2           |
| LLKF_1819  | <i>yrbA</i>      | NAD-dependent oxidoreductase                                          | -0.73           | -0.70           | -0.33           | -2.35           | 0.338           | 0.266           | 0.623           | 0.000           | 2           |
| LLKF_1830  | <i>arb</i>       | 6-phospho-beta-glucosidase                                            | -2.90           | -2.85           | -1.76           | -2.49           | 0.003           | 0.004           | 0.012           | 0.000           | 2           |
| LLKF_1833  | <i>tcsK6</i>     | Two-component system sensor histidine kinase                          | -0.78           | -1.07           | -0.54           | -1.47           | 0.112           | 0.044           | 0.280           | 0.001           | 2           |
| LLKF_1835  | <i>malR</i>      | Transcriptional regulator, LacI family                                | -0.87           | -0.70           | -0.26           | -1.68           | 0.146           | 0.207           | 0.626           | 0.001           | 2           |
| LLKF_1849  | <i>yrdB</i>      | Hypothetical protein, extracellular, N-terminal fragment (pseudogene) | -0.52           | -0.58           | -0.05           | -1.52           | 0.298           | 0.317           | 0.844           | 0.001           | 2           |
| LLKF_1851  | <i>yrfA</i>      | Transcriptional regulator, ArsR family                                | -0.80           | -0.90           | 0.03            | -2.87           | 0.222           | 0.192           | 0.862           | 0.000           | 2           |
| LLKF_1852  | <i>yrfB</i>      | NADH-dependent oxidoreductase                                         | -0.37           | -0.43           | -0.11           | -3.03           | 0.238           | 0.215           | 0.697           | 0.000           | 2           |
| LLKF_1884  | <i>yrgH</i>      | Muramoyltetrapeptide carboxypeptidase                                 | -2.14           | -2.28           | -1.40           | -2.93           | 0.009           | 0.010           | 0.035           | 0.000           | 2           |
| LLKF_1885  | <i>yrgI</i>      | Phosphoglycerate mutase family protein                                | -2.66           | -3.28           | -1.70           | -2.71           | 0.001           | 0.000           | 0.004           | 0.000           | 2           |
| LLKF_1901  | <i>yriC</i>      | Alpha/beta hydrolase                                                  | -1.27           | -0.98           | -0.30           | -1.69           | 0.042           | 0.090           | 0.604           | 0.001           | 2           |
| LLKF_1903  | <i>yriA</i>      | Hydrolase, HAD superfamily                                            | -0.68           | -0.88           | -0.68           | -2.08           | 0.211           | 0.262           | 0.314           | 0.000           | 2           |
| LLKF_1920  | <i>ysaB</i>      | ABC transporter, permease and substrate binding protein               | -0.63           | -0.65           | 0.22            | -1.91           | 0.287           | 0.273           | 0.778           | 0.001           | 2           |
| LLKF_1921  | <i>ysaC</i>      | ABC transporter, ATP-binding protein                                  | -0.84           | -0.84           | 0.04            | -1.70           | 0.155           | 0.193           | 0.822           | 0.001           | 2           |
| LLKF_1924  | <i>aroC</i>      | Chorismate synthase                                                   | -1.79           | -1.77           | -1.07           | -3.02           | 0.009           | 0.011           | 0.069           | 0.000           | 2           |
| LLKF_1935  | <i>atpC</i>      | ATP synthase F1, epsilon subunit                                      | -0.63           | -0.90           | -0.01           | -2.60           | 0.261           | 0.094           | 0.923           | 0.000           | 2           |
| LLKF_1936  | <i>atpD</i>      | ATP synthase F1, beta subunit                                         | -0.37           | -0.51           | 0.05            | -1.80           | 0.603           | 0.452           | 0.912           | 0.000           | 2           |
| LLKF_1943  | <i>estA</i>      | Tributylin esterase                                                   | -1.05           | -0.44           | -0.31           | -2.37           | 0.030           | 0.299           | 0.515           | 0.000           | 2           |
| LLKF_1980  |                  | Hypothetical protein                                                  | -0.73           | -1.61           | -1.65           | -3.07           | 0.237           | 0.026           | 0.017           | 0.000           | 2           |
| LLKF_1981  | <i>adhA</i>      | Alcohol dehydrogenase 1                                               | -1.70           | -1.65           | -1.67           | -4.00           | 0.080           | 0.067           | 0.063           | 0.000           | 2           |
| LLKF_2045  | <i>yticA</i>     | Hypothetical protein                                                  | -1.12           | -1.31           | -0.14           | -1.78           | 0.097           | 0.042           | 0.836           | 0.001           | 2           |
| LLKF_2047  | <i>yticB</i>     | Hypothetical protein                                                  | -2.09           | -2.36           | -0.36           | -1.65           | 0.005           | 0.003           | 0.533           | 0.001           | 2           |
| LLKF_2059  | <i>ytdD</i>      | Hypothetical protein                                                  | -0.78           | -0.82           | 0.09            | -1.83           | 0.162           | 0.137           | 0.896           | 0.000           | 2           |
| LLKF_2060  | <i>ytdE</i>      | Hypothetical protein                                                  | -1.13           | -1.15           | -0.08           | -1.70           | 0.030           | 0.036           | 0.883           | 0.000           | 2           |
| LLKF_2061  | <i>ytdF</i>      | Pyridoxal-5'-phosphate family protein                                 | -1.06           | -1.16           | -0.14           | -1.56           | 0.043           | 0.029           | 0.813           | 0.000           | 2           |
| LLKF_2094  | <i>ytgG</i>      | Glucosamine-6-phosphate isomerase                                     | -1.21           | -0.75           | -0.20           | -1.94           | 0.040           | 0.164           | 0.724           | 0.000           | 2           |
| LLKF_2110  | <i>cbiA/cglA</i> | Cystathionine beta-lyase                                              | -2.23           | -2.73           | -0.06           | -2.05           | 0.003           | 0.001           | 0.886           | 0.000           | 2           |
| LLKF_2111  | <i>cgs</i>       | Cystathionine gamma-synthase                                          | -1.71           | -2.19           | 0.40            | -1.91           | 0.028           | 0.008           | 0.496           | 0.000           | 2           |
| LLKF_2112  | <i>metA</i>      | Homoserine O-succinyltransferase                                      | -1.50           | -1.92           | 0.09            | -1.74           | 0.091           | 0.010           | 0.728           | 0.001           | 2           |
| LLKF_2186  |                  | Hypothetical protein                                                  | -0.99           | -0.95           | -0.30           | -2.50           | 0.181           | 0.263           | 0.662           | 0.000           | 2           |
| LLKF_2191  | <i>yuiB</i>      | Hypothetical protein                                                  | -1.92           | -1.99           | -1.62           | -2.94           | 0.037           | 0.062           | 0.027           | 0.000           | 2           |
| LLKF_2192  | <i>pmsR</i>      | Peptide methionine sulfoxide reductase                                | -1.76           | -1.61           | -1.23           | -2.97           | 0.011           | 0.016           | 0.035           | 0.000           | 2           |
| LLKF_2198  | <i>ackA2</i>     | Acetate kinase                                                        | -2.59           | -2.70           | -0.93           | -4.30           | 0.005           | 0.004           | 0.128           | 0.000           | 2           |
| LLKF_2292  | <i>yvdB</i>      | Hypothetical protein                                                  | -1.03           | -1.22           | -0.32           | -2.24           | 0.210           | 0.051           | 0.583           | 0.000           | 2           |
| LLKF_2293  | <i>yvdC</i>      | CAAX amino terminal protease family protein                           | -0.85           | -1.11           | -0.47           | -2.45           | 0.143           | 0.058           | 0.420           | 0.000           | 2           |

| Feature ID | Gene         | Annotation                                                                  | NZ5521_s<br>tat | NZ5522_s<br>tat | NZ5523_s<br>tat | _IL594_s<br>tat | NZ5521_s<br>tat | NZ5522_s<br>tat | NZ5523_s<br>tat | _IL594_s<br>tat | Clust<br>er |
|------------|--------------|-----------------------------------------------------------------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-------------|
| LLKF_2357  | <i>pbp2A</i> | Multimodular transpeptidase-transglycosylase Pbp2A                          | -1.11           | -0.97           | -0.70           | -2.03           | 0.082           | 0.143           | 0.225           | 0.000           | 2           |
| LLKF_2399  | <i>ywdA</i>  | Hypothetical protein                                                        | -0.69           | -0.68           | -0.23           | -1.81           | 0.393           | 0.322           | 0.742           | 0.001           | 2           |
| LLKF_2486  | <i>ywjH</i>  | Hypothetical protein                                                        | -0.50           | -0.58           | 0.26            | -1.81           | 0.306           | 0.233           | 0.646           | 0.000           | 2           |
| LLKF_2489  | <i>zwf</i>   | Glucose-6-phosphate 1-dehydrogenase                                         | -1.41           | -1.22           | -0.37           | -1.66           | 0.022           | 0.056           | 0.538           | 0.001           | 2           |
| LLKF_2522  | <i>yxeA</i>  | ABC transporter, permease protein                                           | -1.15           | -1.17           | -0.33           | -2.51           | 0.032           | 0.033           | 0.543           | 0.000           | 2           |
| LLKF_2523  | <i>yxeB</i>  | ABC transporter, ATP-binding protein                                        | -1.21           | -0.91           | -0.80           | -1.96           | 0.040           | 0.117           | 0.131           | 0.001           | 2           |
| LLKF_0053  | <i>yahl</i>  | Short chain dehydrogenase                                                   | -0.37           | -0.26           | 0.24            | -2.08           | 0.164           | 0.276           | 0.692           | 0.000           | 3           |
| LLKF_0188  | <i>ybjB</i>  | Hypothetical protein                                                        | -0.19           | 0.00            | 0.23            | -1.39           | 0.680           | 0.586           | 0.673           | 0.001           | 3           |
| LLKF_0355  | <i>napC</i>  | Multidrug-efflux transporter, MF superfamily                                | 1.78            | 2.68            | -0.55           | -2.20           | 0.036           | 0.005           | 0.432           | 0.001           | 3           |
| LLKF_0528  | <i>yfdG</i>  | Hypothetical protein                                                        | 0.19            | 0.24            | -0.52           | -1.49           | 0.687           | 0.609           | 0.301           | 0.001           | 3           |
| LLKF_0556  | <i>yfhB</i>  | Hypothetical protein                                                        | 0.08            | 0.20            | -0.13           | -1.83           | 0.825           | 0.543           | 0.830           | 0.000           | 3           |
| LLKF_0558  | <i>tpsO</i>  | Regulatory protein, TpsO family                                             | 0.65            | 1.15            | 0.13            | -2.22           | 0.331           | 0.064           | 0.761           | 0.000           | 3           |
| LLKF_0559  | <i>yfhF</i>  | Hypothetical protein                                                        | 0.25            | 0.42            | 0.11            | -2.10           | 0.606           | 0.425           | 0.786           | 0.000           | 3           |
| LLKF_0560  | <i>yfhG</i>  | Dihydroxyacetone kinase family protein                                      | 0.45            | 0.53            | -0.17           | -2.09           | 0.384           | 0.329           | 0.707           | 0.000           | 3           |
| LLKF_0561  | <i>yfhH</i>  | Hypothetical protein                                                        | 0.15            | 0.30            | -0.35           | -2.51           | 0.428           | 0.407           | 0.501           | 0.000           | 3           |
| LLKF_0562  | <i>yfhI</i>  | Hypothetical protein                                                        | 0.09            | 0.35            | -0.33           | -2.21           | 0.640           | 0.428           | 0.568           | 0.000           | 3           |
| LLKF_0563  | <i>yfhJ</i>  | Glyoxalase family protein                                                   | 0.11            | 0.57            | -0.04           | -1.87           | 0.640           | 0.354           | 0.964           | 0.000           | 3           |
| LLKF_0564  | <i>yfhK</i>  | Hypothetical protein                                                        | -0.35           | -0.30           | -0.57           | -2.03           | 0.530           | 0.494           | 0.330           | 0.000           | 3           |
| LLKF_0588  | <i>yjiF</i>  | Multidrug transporter, MF superfamily                                       | 1.08            | 1.11            | 0.33            | -2.00           | 0.034           | 0.034           | 0.525           | 0.000           | 3           |
| LLKF_0655  | <i>ygiG</i>  | Acetyltransferase, GNAT family                                              | 1.50            | 0.72            | 0.21            | -2.89           | 0.028           | 0.227           | 0.743           | 0.000           | 3           |
| LLKF_0656  | <i>ygiH</i>  | Hypothetical protein                                                        | 1.73            | 1.02            | 0.31            | -1.82           | 0.014           | 0.090           | 0.648           | 0.001           | 3           |
| LLKF_1003  | <i>nrpF</i>  | Ribonucleoside-diphosphate reductase, beta chain                            | 0.11            | 0.46            | -0.55           | -1.92           | 0.825           | 0.366           | 0.294           | 0.000           | 3           |
| LLKF_1004  | <i>nrpE</i>  | Ribonucleoside-diphosphate reductase, alpha chain                           | -0.49           | -0.06           | -0.69           | -1.92           | 0.423           | 0.771           | 0.211           | 0.000           | 3           |
| LLKF_1082  | <i>pp153</i> | Phage protein, tail component                                               | 0.14            | -0.02           | 0.11            | -2.64           | 0.801           | 0.968           | 0.883           | 0.000           | 3           |
| LLKF_1083  | <i>pp154</i> | Phage protein, receptor-binding protein                                     | 0.90            | 0.68            | 0.19            | -2.11           | 0.124           | 0.228           | 0.784           | 0.000           | 3           |
| LLKF_1110  | <i>mntH1</i> | Manganese transport protein MntH, Nramp family                              | 0.29            | 0.81            | 1.44            | -3.76           | 0.403           | 0.143           | 0.012           | 0.000           | 3           |
| LLKF_1243  | <i>ymcE</i>  | Transcriptional regulator, Xre family                                       | 0.31            | -0.15           | 0.51            | -1.74           | 0.609           | 0.492           | 0.321           | 0.000           | 3           |
| LLKF_1244  | <i>ymcF</i>  | Mucus-binding protein, N-terminal fragment (pseudogene)                     | 0.49            | -0.02           | 0.94            | -2.29           | 0.371           | 0.821           | 0.109           | 0.000           | 3           |
| LLKF_1317  | <i>lctO</i>  | L-lactate oxidase                                                           | 1.35            | 1.86            | 0.32            | -4.93           | 0.022           | 0.007           | 0.575           | 0.000           | 3           |
| LLKF_1340  | <i>ynaE</i>  | Riboflavin transporter                                                      | 1.43            | 0.55            | -0.14           | -1.80           | 0.324           | 0.245           | 0.711           | 0.000           | 3           |
| LLKF_1566  | <i>trpA</i>  | Tryptophan synthase, alpha chain                                            | -0.11           | -0.38           | -0.33           | -1.88           | 0.871           | 0.560           | 0.660           | 0.001           | 3           |
| LLKF_1576  |              | Bifunctional protein: Nitroreductase/Transcriptional regulator, MarR family | -0.35           | -0.23           | -0.62           | -2.33           | 0.514           | 0.672           | 0.258           | 0.000           | 3           |
| LLKF_1863  |              | Transcriptional regulator, LuxR family                                      | 0.39            | 0.62            | -0.31           | -1.79           | 0.409           | 0.191           | 0.562           | 0.000           | 3           |
| LLKF_1937  | <i>atpG</i>  | ATP synthase F1, gamma subunit                                              | -0.18           | -0.18           | 0.11            | -1.54           | 0.533           | 0.589           | 0.851           | 0.001           | 3           |
| LLKF_2009  | <i>ysiC</i>  | Acetyltransferase, GNAT family                                              | 0.66            | 0.65            | -0.64           | -2.22           | 0.140           | 0.144           | 0.155           | 0.000           | 3           |
| LLKF_2216  | <i>yvaD</i>  | Hypothetical protein                                                        | 0.41            | 0.69            | -0.61           | -1.52           | 0.459           | 0.263           | 0.270           | 0.001           | 3           |
| LLKF_2217  | <i>arcD2</i> | Arginine/ornithine antiporter                                               | 0.86            | 0.81            | -0.38           | -1.41           | 0.086           | 0.090           | 0.413           | 0.001           | 3           |
| LLKF_2224  | <i>argS</i>  | Arginyl-tRNA synthetase                                                     | -0.08           | -0.44           | -0.16           | -1.65           | 0.812           | 0.361           | 0.744           | 0.000           | 3           |
| LLKF_2290  | <i>poxL</i>  | Pyruvate oxidase                                                            | 1.93            | 2.45            | 0.39            | -2.89           | 0.020           | 0.006           | 0.517           | 0.001           | 3           |
| LLKF_0061  | <i>cdaA</i>  | Lead, cadmium, zinc, mercury transporting ATPase                            | -0.31           | 0.31            | 0.02            | 2.11            | 0.553           | 0.565           | 0.957           | 0.000           | 4           |

| Feature ID | Gene             | Annotation                                                              | NZ5521_s<br>tat | NZ5522_s<br>tat | NZ5523_s<br>tat | _IL594_s<br>tat | NZ5521_s<br>tat | NZ5522_s<br>tat | NZ5523_s<br>tat | IL594_s<br>tat | Clust<br>er |
|------------|------------------|-------------------------------------------------------------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|----------------|-------------|
| LLKF_0127  | <i>ybeF-N</i>    | Collagen adhesion protein, N-terminus (pseudogene)                      | 0.46            | 0.30            | 0.57            | 3.68            | 0.380           | 0.396           | 0.414           | 0.000          | 4           |
| LLKF_0245  | <i>dhaK</i>      | PTS-dependent dihydroxyacetone kinase, dihydroxyacetone-binding subunit | -1.36           | -1.80           | -3.01           | 3.72            | 0.063           | 0.027           | 0.002           | 0.000          | 4           |
| LLKF_0246  | <i>dhaL</i>      | PTS-dependent dihydroxyacetone kinase, ADP-binding subunit              | -0.81           | -0.74           | -2.57           | 4.11            | 0.368           | 0.315           | 0.003           | 0.000          | 4           |
| LLKF_0247  | <i>dhaM</i>      | PTS-dependent dihydroxyacetone kinase, phosphotransferase subunit       | -1.07           | -1.02           | -2.48           | 3.88            | 0.211           | 0.245           | 0.003           | 0.000          | 4           |
| LLKF_0248  | <i>glpF1</i>     | Glycerol uptake facilitator protein                                     | -0.65           | -0.88           | -2.57           | 3.56            | 0.449           | 0.318           | 0.004           | 0.000          | 4           |
| LLKF_0250  | <i>ycfA</i>      | Transcriptional regulator, TetR family                                  | -0.46           | 0.12            | -0.22           | 2.32            | 0.413           | 0.682           | 0.741           | 0.000          | 4           |
| LLKF_0346  | <i>ycjG</i>      | Hypothetical protein                                                    | -0.32           | -0.55           | -0.28           | 2.12            | 0.481           | 0.229           | 0.597           | 0.000          | 4           |
| LLKF_0427  | <i>ldhB</i>      | L-lactate dehydrogenase                                                 | 0.71            | 0.95            | -0.09           | 3.48            | 0.266           | 0.130           | 0.815           | 0.000          | 4           |
| LLKF_0619  | <i>ygbB</i>      | Hypothetical protein                                                    | 0.48            | -0.32           | -1.10           | 1.85            | 0.410           | 0.572           | 0.184           | 0.001          | 4           |
| LLKF_0801  | <i>cbiB/cglB</i> | Cystathionine beta-lyase / Cystathionine gamma-lyase                    | -0.50           | -0.83           | -1.59           | 5.12            | 0.449           | 0.228           | 0.027           | 0.000          | 4           |
| LLKF_0802  | <i>cysK1</i>     | Cysteine synthase                                                       | -0.16           | -0.65           | -1.76           | 5.14            | 0.835           | 0.352           | 0.022           | 0.000          | 4           |
| LLKF_1189  | <i>potA</i>      | Spermidine/putrescine ABC transporter, ATP-binding protein PotA         | -0.37           | -0.25           | -0.78           | 1.63            | 0.457           | 0.492           | 0.116           | 0.000          | 4           |
| LLKF_1389  | <i>yneB</i>      | Esterase/lipase                                                         | 0.52            | 0.58            | 0.14            | 3.60            | 0.315           | 0.269           | 0.839           | 0.000          | 4           |
| LLKF_1390  | <i>yneC</i>      | Hypothetical protein                                                    | 0.94            | 0.78            | 0.18            | 4.03            | 0.081           | 0.141           | 0.798           | 0.000          | 4           |
| LLKF_1542  | <i>yogA</i>      | Hypothetical protein                                                    | -0.44           | -0.96           | -1.55           | 2.98            | 0.535           | 0.156           | 0.011           | 0.000          | 4           |
| LLKF_1629  | <i>xylA</i>      | Xylose isomerase                                                        | -0.23           | 0.04            | -0.78           | 3.53            | 0.585           | 0.488           | 0.240           | 0.000          | 4           |
| LLKF_1792  | <i>rbsB</i>      | Ribose ABC transporter, substrate binding protein                       | 0.25            | 0.23            | -0.11           | 3.66            | 0.579           | 0.350           | 0.823           | 0.000          | 4           |
| LLKF_1793  | <i>rbsC</i>      | Ribose ABC transporter, permease protein                                | -0.21           | -0.34           | -0.32           | 3.79            | 0.601           | 0.648           | 0.624           | 0.000          | 4           |
| LLKF_1797  | <i>rbsR</i>      | Ribose operon repressor                                                 | -0.06           | -0.37           | -0.78           | 4.75            | 0.524           | 0.290           | 0.246           | 0.000          | 4           |
| LLKF_1925  | <i>ysbA</i>      | Hydrolase, HAD superfamily                                              | -1.07           | -1.04           | -0.23           | 1.88            | 0.083           | 0.182           | 0.700           | 0.001          | 4           |
| LLKF_1976  | <i>pepO</i>      | Oligoendopeptidase O                                                    | -1.08           | -1.57           | -0.69           | 1.92            | 0.068           | 0.017           | 0.200           | 0.000          | 4           |
| LLKF_2273  |                  | IS981 transposase B                                                     | 0.09            | -0.54           | -2.06           | 3.23            | 0.836           | 0.558           | 0.033           | 0.000          | 4           |
| LLKF_2274  |                  | IS981 transposase A                                                     | 0.42            | -0.81           | -3.25           | 3.69            | 0.547           | 0.401           | 0.004           | 0.000          | 4           |
| LLKF_2276  |                  | IS981 transposase B                                                     | 0.09            | -0.54           | -2.06           | 3.23            | 0.836           | 0.558           | 0.033           | 0.000          | 4           |
| LLKF_2277  |                  | IS981 transposase A                                                     | 0.42            | -0.81           | -3.25           | 3.69            | 0.547           | 0.401           | 0.004           | 0.000          | 4           |
| LLKF_0108  | <i>argG</i>      | Argininosuccinate synthase                                              | -3.25           | -2.81           | -3.09           | -6.01           | 0.010           | 0.021           | 0.008           | 0.000          | 5           |
| LLKF_0167  | <i>celB</i>      | PTS system, cellobiose-specific IIC component                           | -2.96           | -3.77           | -2.84           | -5.12           | 0.005           | 0.001           | 0.003           | 0.000          | 5           |
| LLKF_0280  | <i>ymgG</i>      | General stress protein, Gls24 family                                    | -1.45           | -4.96           | -2.84           | -5.94           | 0.064           | 0.000           | 0.003           | 0.000          | 5           |
| LLKF_0541  | <i>gltS</i>      | Glutamate or arginine ABC transporter, substrate binding protein        | -2.79           | -2.22           | -2.26           | -5.94           | 0.008           | 0.023           | 0.015           | 0.000          | 5           |
| LLKF_0542  | <i>argE</i>      | Acetylornithine deacetylase                                             | -2.86           | -2.53           | -2.39           | -6.37           | 0.007           | 0.012           | 0.008           | 0.000          | 5           |
| LLKF_0817  | <i>argC</i>      | N-acetyl-gamma-glutamyl-phosphate reductase                             | -2.09           | -0.78           | -3.66           | -4.76           | 0.051           | 0.427           | 0.004           | 0.000          | 5           |
| LLKF_0818  | <i>argJ</i>      | Glutamate N-acetyltransferase                                           | -2.26           | -1.24           | -4.10           | -5.03           | 0.069           | 0.275           | 0.005           | 0.000          | 5           |
| LLKF_0819  | <i>argD</i>      | Acetylornithine aminotransferase                                        | -1.77           | -1.07           | -3.75           | -3.93           | 0.121           | 0.288           | 0.003           | 0.000          | 5           |
| LLKF_0820  | <i>argB</i>      | Acetylglutamate kinase                                                  | -2.04           | -1.32           | -3.56           | -4.19           | 0.039           | 0.146           | 0.003           | 0.000          | 5           |
| LLKF_0821  | <i>argF</i>      | Ornithine carbamoyltransferase                                          | -2.09           | -1.34           | -3.67           | -4.48           | 0.060           | 0.196           | 0.004           | 0.000          | 5           |
| LLKF_1319  | <i>metF</i>      | Methylenetetrahydrofolate reductase                                     | -3.07           | -3.74           | -1.57           | -5.86           | 0.004           | 0.002           | 0.044           | 0.000          | 5           |
| LLKF_1320  | <i>metE</i>      | 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase   | -2.77           | -3.10           | -1.19           | -5.30           | 0.006           | 0.004           | 0.121           | 0.000          | 5           |
| LLKF_1969  | <i>ysfE</i>      | Polar amino acid ABC transporter, ATP-binding protein protein           | -1.85           | -1.41           | -2.43           | -5.99           | 0.046           | 0.126           | 0.010           | 0.000          | 5           |
| LLKF_1970  | <i>ysfF</i>      | Polar amino acid ABC transporter, permease protein                      | -2.03           | -1.76           | -1.71           | -5.28           | 0.034           | 0.063           | 0.045           | 0.000          | 5           |

| Feature ID | Gene         | Annotation                                             | NZ5521_s<br>tat | NZ5522_s<br>tat | NZ5523_s<br>tat | _IL594_s<br>tat | NZ5521_s<br>tat | NZ5522_s<br>tat | NZ5523_s<br>tat | _IL594_s<br>tat | Clust<br>er |
|------------|--------------|--------------------------------------------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-------------|
| LLKF_2163  | <i>galE</i>  | UDP-glucose 4-epimerase                                | -4.43           | -4.80           | -1.01           | -3.38           | 0.000           | 0.000           | 0.037           | 0.000           | 5           |
| LLKF_2164  | <i>lacZ</i>  | Beta-galactosidase                                     | -4.57           | -4.86           | -1.29           | -4.04           | 0.000           | 0.000           | 0.039           | 0.000           | 5           |
| LLKF_2165  | <i>thgA</i>  | Galactoside O-acetyltransferase                        | -3.88           | -4.40           | -1.27           | -3.28           | 0.000           | 0.000           | 0.019           | 0.000           | 5           |
| LLKF_2166  | <i>galT1</i> | Galactose-1-phosphate uridylyltransferase              | -4.14           | -4.58           | -1.70           | -3.17           | 0.000           | 0.000           | 0.011           | 0.000           | 5           |
| LLKF_2167  | <i>galK1</i> | Galactokinase                                          | -4.32           | -4.71           | -1.56           | -2.64           | 0.000           | 0.000           | 0.015           | 0.000           | 5           |
| LLKF_2168  | <i>galM1</i> | Aldose 1-epimerase                                     | -4.38           | -4.81           | -1.35           | -3.02           | 0.000           | 0.000           | 0.014           | 0.000           | 5           |
| LLKF_2169  | <i>lacS</i>  | Lactose permease                                       | -3.89           | -4.52           | -1.31           | -2.83           | 0.001           | 0.000           | 0.051           | 0.000           | 5           |
| LLKF_0518  | <i>cysK2</i> | Cysteine synthase                                      | 0.63            | 0.50            | -0.71           | 4.99            | 0.255           | 0.372           | 0.225           | 0.000           | 6           |
| LLKF_1794  | <i>rbsA</i>  | Ribose ABC transporter, ATP-binding protein            | 0.65            | 0.31            | -0.02           | 4.88            | 0.157           | 0.224           | 0.673           | 0.000           | 6           |
| LLKF_1795  | <i>rbsD</i>  | D-ribose mutarotase                                    | 0.55            | 0.14            | -0.20           | 5.45            | 0.258           | 0.787           | 0.743           | 0.000           | 6           |
| LLKF_1796  | <i>rbsK</i>  | Ribokinase                                             | 0.44            | 0.15            | -0.20           | 5.12            | 0.467           | 0.634           | 0.664           | 0.000           | 6           |
| LLKF_1898  | <i>pepF</i>  | Oligoendopeptidase F                                   | 1.48            | 1.31            | -0.22           | 4.18            | 0.039           | 0.064           | 0.783           | 0.000           | 6           |
| LLKF_1974  | <i>codY</i>  | Transcription pleiotropic repressor codY               | 1.77            | 1.51            | 0.55            | 5.14            | 0.023           | 0.040           | 0.449           | 0.000           | 6           |
| LLKF_1975  | <i>ysgA</i>  | Transcriptional regulator                              | 1.81            | 1.50            | 0.20            | 5.42            | 0.014           | 0.026           | 0.591           | 0.000           | 6           |
| LLKF_2031  | <i>oppB</i>  | Oligopeptide ABC transporter, permease protein OppB    | 2.38            | 2.92            | -0.16           | 8.54            | 0.026           | 0.013           | 0.906           | 0.000           | 6           |
| LLKF_2032  | <i>oppF</i>  | Oligopeptide ABC transporter, ATP-binding protein OppF | 2.55            | 2.80            | 0.05            | 8.56            | 0.020           | 0.015           | 0.969           | 0.000           | 6           |
| LLKF_2033  | <i>oppD</i>  | Oligopeptide ABC transporter, ATP-binding protein OppD | 2.26            | 2.66            | 0.24            | 8.09            | 0.029           | 0.017           | 0.841           | 0.000           | 6           |
| LLKF_2426  | <i>ywfG</i>  | Mucus-binding protein, LPXTG-anchored                  | 0.57            | 0.56            | 0.42            | 6.72            | 0.559           | 0.467           | 0.600           | 0.000           | 6           |
| LLKF_0537  | <i>gapA</i>  | Glyceraldehyde 3-phosphate dehydrogenase               | 3.51            | 4.06            | 0.26            | 4.56            | 0.010           | 0.007           | 0.637           | 0.000           | 7           |
| LLKF_0846  | <i>copA</i>  | Copper-translocating P-type ATPase                     | 4.60            | 4.85            | 0.71            | 2.82            | 0.005           | 0.004           | 0.353           | 0.001           | 7           |
| LLKF_0870  | <i>copB</i>  | Copper-translocating P-type ATPase                     | 5.39            | 5.49            | 1.20            | 2.57            | 0.000           | 0.000           | 0.021           | 0.000           | 7           |
| LLKF_0983  | <i>dnaK</i>  | Chaperone protein dnaK                                 | 3.44            | 3.55            | 1.03            | 3.23            | 0.011           | 0.010           | 0.291           | 0.001           | 7           |
| LLKF_1170  | <i>guaC</i>  | GMP reductase                                          | 4.54            | 3.49            | 0.98            | 4.44            | 0.000           | 0.000           | 0.049           | 0.000           | 7           |
| LLKF_1644  | <i>clpB</i>  | ATP-dependent Clp protease, chaperonin ATPase ClpB     | 6.14            | 6.25            | -0.93           | 5.16            | 0.003           | 0.004           | 0.475           | 0.000           | 7           |
| LLKF_2051  | <i>uspA3</i> | Universal stress protein A                             | 4.00            | 4.24            | 0.54            | 2.89            | 0.000           | 0.000           | 0.420           | 0.000           | 7           |
| LLKF_2417  | <i>yweE</i>  | Transcriptional regulator, MarR family                 | 4.62            | 4.12            | 0.61            | 3.67            | 0.002           | 0.003           | 0.575           | 0.000           | 7           |
| LLKF_2470  | <i>glnA</i>  | Glutamine synthetase                                   | 4.18            | 3.38            | 0.32            | 3.25            | 0.001           | 0.002           | 0.641           | 0.000           | 7           |
| LLKF_2471  | <i>glnR</i>  | Transcriptional regulator, MerR family                 | 3.94            | 3.03            | 0.26            | 3.46            | 0.001           | 0.002           | 0.741           | 0.000           | 7           |
| LLKF_2502  | <i>yxbD</i>  | Transporter, MFS superfamily                           | 2.05            | 2.00            | 6.35            | 5.73            | 0.030           | 0.019           | 0.000           | 0.000           | 8           |
| LLKF_2503  | <i>uspA4</i> | Universal stress protein A                             | 3.05            | 2.37            | 7.09            | 6.31            | 0.004           | 0.014           | 0.000           | 0.000           | 8           |
| LLKF_2504  | <i>yxbF</i>  | Hypothetical protein                                   | 3.14            | 2.53            | 6.98            | 6.87            | 0.007           | 0.016           | 0.000           | 0.000           | 8           |

## Supplemental References

- Barrick JE, Yu DS, Yoon SH, Jeong H, Oh TK, Schneider D, Lenski RE, Kim JF. 2009. Genome evolution and adaptation in a long-term experiment with *Escherichia coli*. *Nature* **461**(7268): 1243-1247.
- Bockelmann W, Monnet V, Geis A, Teuber M, Gripon JC. 1989. Comparison of cell wall proteinases from *Lactococcus lactis* subsp. *cremoris* AC1 and *Lactococcus lactis* subsp. *lactis* NCDO 763 *Applied Microbiology and Biotechnology* **31**(3): 278-282.
- Bolotin A, Wincker P, Mauger S, Jaillon O, Malarne K, Weissenbach J, Ehrlich SD, Sorokin A. 2001. The complete genome sequence of the lactic acid bacterium *Lactococcus lactis* ssp. *lactis* IL1403. *Genome Res* **11**(5): 731-753.
- Chopin A, Chopin MC, Moillo-Batt A, Langella P. 1984. Two plasmid-determined restriction and modification systems in *Streptococcus lactis*. *Plasmid* **11**(3): 260-263.
- Christensson C, Pillidge CJ, Ward LJ, O'Toole PW. 2001. Nucleotide sequence and characterization of the cell envelope proteinase plasmid in *Lactococcus lactis* subsp. *cremoris* HP. *J Appl Microbiol* **91**(2): 334-343.
- de Vos WM, Vos P, de Haard H, Boerrigter I. 1989. Cloning and expression of the *Lactococcus lactis* subsp. *cremoris* SK11 gene encoding an extracellular serine proteinase. *Gene* **85**(1): 169-176.
- Exterkate FA, Alting AC, Bruinenberg PG. 1993. Diversity of cell envelope proteinase specificity among strains of *Lactococcus lactis* and its relationship to charge characteristics of the substrate-binding region. *Applied and environmental microbiology* **59**(11): 3640-3647.

- Gasson MJ. 1983. Plasmid complements of *Streptococcus lactis* NCDO 712 and other lactic streptococci after protoplast-induced curing. *J Bacteriol* **154**(1): 1-9.
- Kiwaki M, Ikemura H, Shimizu-Kadota M, Hirashima A. 1989. Molecular characterization of a cell wall-associated proteinase gene from *Streptococcus lactis* NCDO763. *Mol Microbiol* **3**(3): 359-369.
- Kok J, Leenhouts KJ, Haandrikman AJ, Ledeboer AM, Venema G. 1988. Nucleotide sequence of the cell wall proteinase gene of *Streptococcus cremoris* Wg2. *Applied and environmental microbiology* **54**(1): 231-238.
- Kunji ER, Mierau I, Hagting A, Poolman B, Konings WN. 1996. The proteolytic systems of lactic acid bacteria. *Antonie Van Leeuwenhoek* **70**(2-4): 187-221.
- Makarova K, Slesarev A, Wolf Y, Sorokin A, Mirkin B, Koonin E, Pavlov A, Pavlova N, Karamychev V, Polouchine N et al. 2006. Comparative genomics of the lactic acid bacteria. *Proc Natl Acad Sci U S A* **103**(42): 15611-15616.
- Rademaker JL, Herbet H, Starrenburg MJ, Naser SM, Gevers D, Kelly WJ, Hugenholtz J, Swings J, van Hylckama Vlieg JE. 2007. Diversity analysis of dairy and nondairy *Lactococcus lactis* isolates, using a novel multilocus sequence analysis scheme and (GTG)<sub>5</sub>-PCR fingerprinting. *Appl Environ Microbiol* **73**(22): 7128-7137.
- Ward LJ, Heap HA, Kelly WJ. 2004. Characterization of closely related lactococcal starter strains which show differing patterns of bacteriophage sensitivity. *J Appl Microbiol* **96**(1): 144-148.