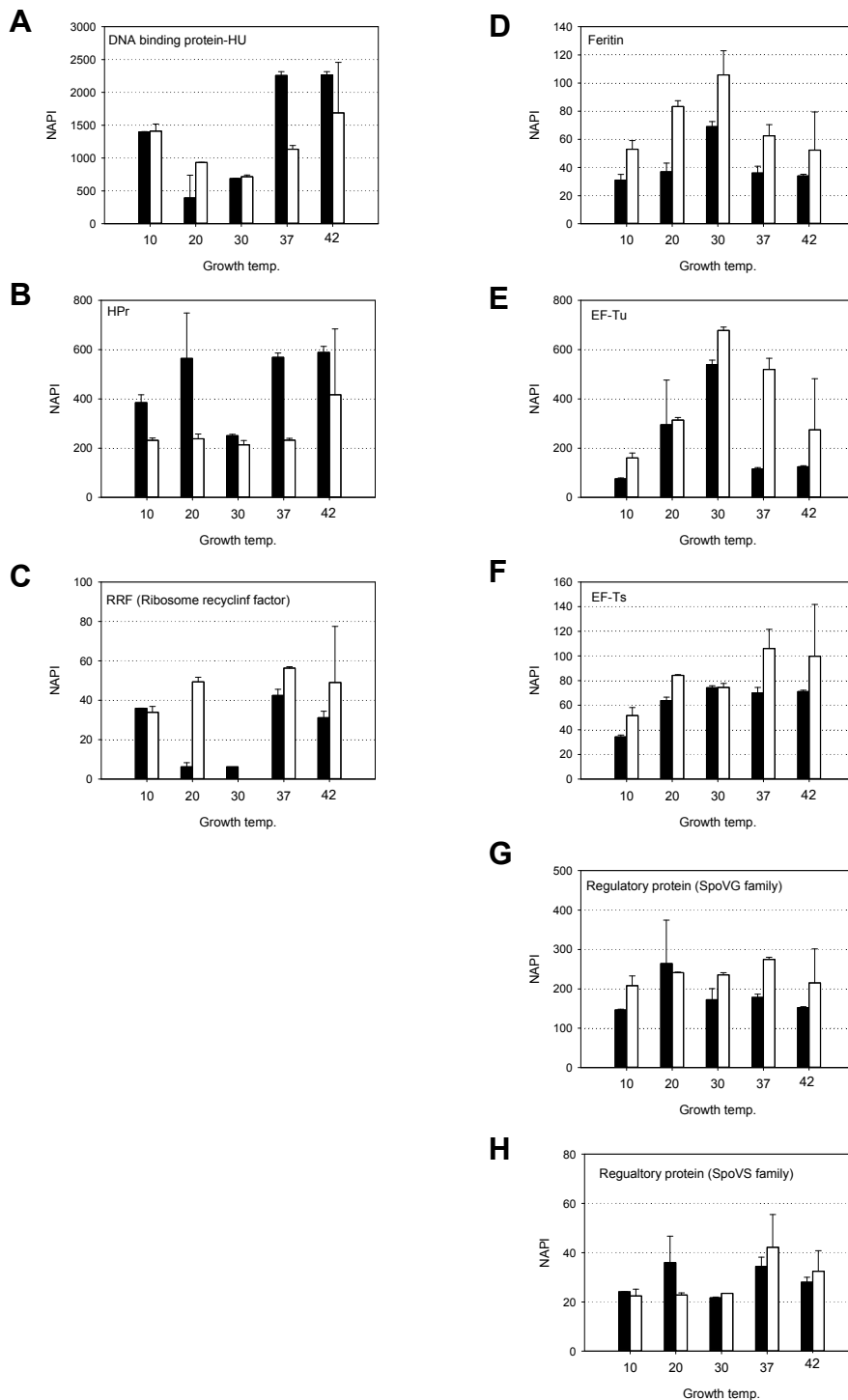
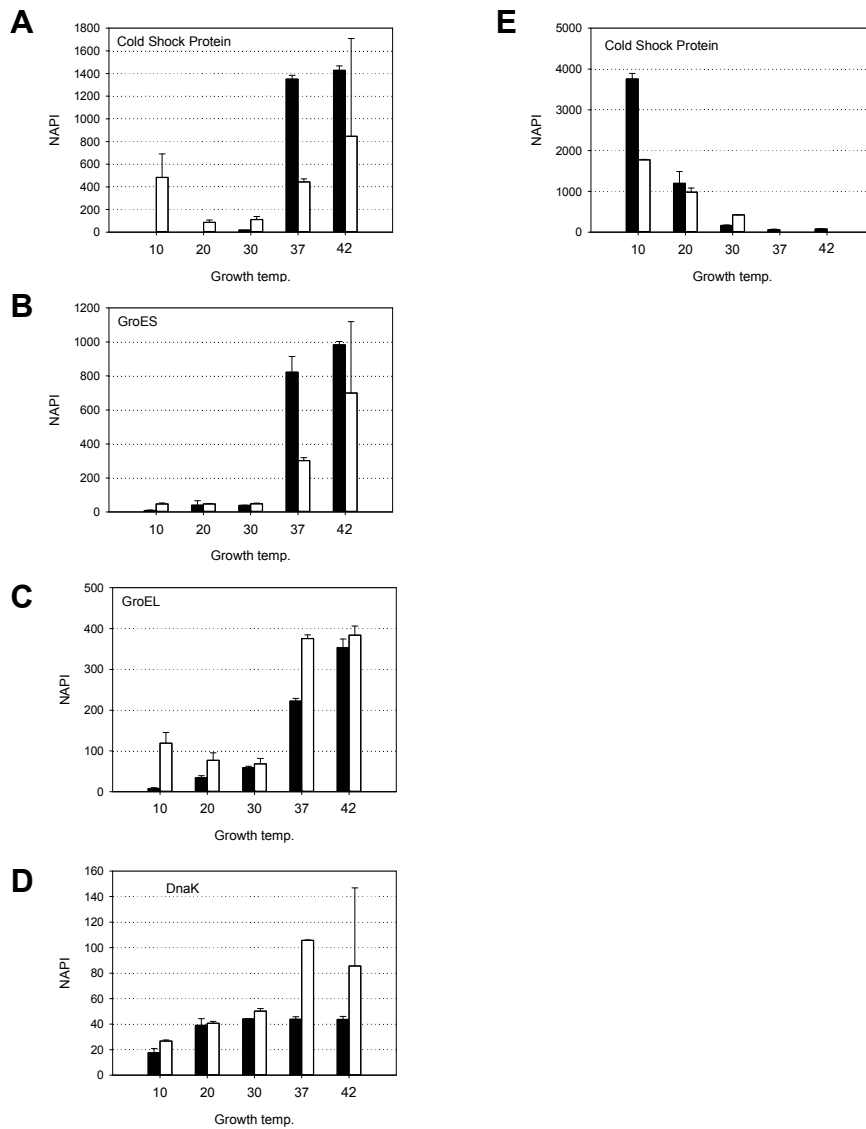


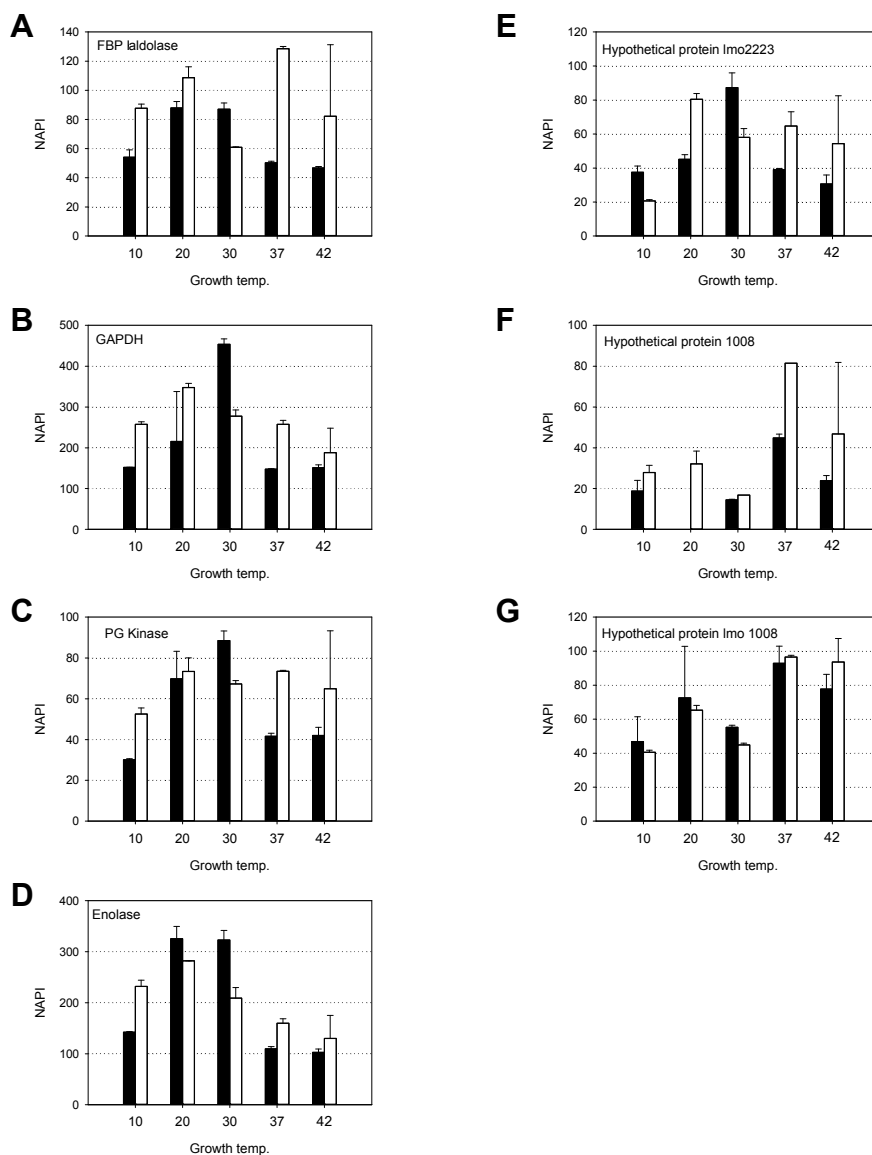
**Supplementary Figure 1** The expression of highly expressed proteins. Group 1: (A) DNA binding protein-HU, (B) phosphor carrier protein HPr (GI: 16803042), (C) RRF (Ribosomal recycling protein, GI: 16803354) (D) Ferritin (non-heme iron-binding, GI: 16802983), (E) EF-Tu (Elongation factor-Tu, GI: 16804690), (F) ET-Ts (Elongation factor-Ts, GI: 16803697), (G) Regulatory protein (SpoVS family: GI 16802242), (H) Regulatory protein (SpoVS family: GI 16802243). Block and white bar indicates the exponential and stationary phase samples, respectively



**Supplementary Figure 2** The expression of highly expressed proteins. Group 2: (A) Cold shock protein (GI 16804055), (B) GroES (GI: 16804108), (C) GroEL (GI: 16804107), (D) DnaK (GI: 16803513), (E) Cold shock protein (GI: 16803404). Block and white bar indicates the exponential and stationary phase samples, respectively



**Supplementary Figure 3** The expression of highly expressed proteins. Group 3: (A) Fructose-6-phosphate aldolase (GI: 16804594), (B) Glyceraldehyde dehydrogenase (GI: 16804497), (C) Phosphoglycerate kinase (GI: 16804496), (D) Enolase (GI: 16804493), (E) Hypothetical protein lmo2223 (GI: 16804262), (F) hypothetical protein lmo1008 (GI: 16803068), (G) hypothetical protein lmo1008 (GI:10683048). Block and white bar indicates the exponential and stationary phase samples, respectively



**Supplementary Table 1.** The summary of proteomics analysis results

| Temperature | Growth phase | Total spectra assigned |      | Total unique assigned |      | Number of identified proteins |     |
|-------------|--------------|------------------------|------|-----------------------|------|-------------------------------|-----|
|             |              | 1 <sup>a</sup>         | 2    | 1                     | 2    | 1                             | 2   |
| 10 °C       | Exponential  | 5220                   | 5157 | 1107                  | 1085 | 367                           | 357 |
|             | Stationary   | 3906                   | 4342 | 1149                  | 1143 | 371                           | 377 |
| 20 °C       | Exponential  | 4931                   | 2688 | 1219                  | 789  | 411                           | 305 |
|             | Stationary   | 4170                   | 3922 | 1172                  | 1111 | 380                           | 375 |
| 30 °C       | Exponential  | 4673                   | 2930 | 1291                  | 976  | 419                           | 360 |
|             | Stationary   | 3670                   | 3662 | 1140                  | 1132 | 385                           | 377 |
| 37 °C       | Exponential  | 5143                   | 5236 | 1009                  | 993  | 346                           | 333 |
|             | Stationary   | 3932                   | 3843 | 1146                  | 1119 | 370                           | 367 |
| 42 °C       | Exponential  | 5625                   | 5561 | 954                   | 943  | 333                           | 317 |
|             | Stationary   | 3906                   | 3888 | 1149                  | 1112 | 371                           | 366 |

<sup>a</sup> Experiments were performed in duplicate. The number means repeat time.

**Supplementary Table 2.** The expression level of top 20 most expressed proteins at 37°C exponential phase.

| Rank <sup>a</sup> | GI <sup>b</sup> | Name         |  | NSAF X 10000 (Ave ± SD) <sup>c</sup> |            |          |           |           |                  |           |          |           |            |
|-------------------|-----------------|--------------|--|--------------------------------------|------------|----------|-----------|-----------|------------------|-----------|----------|-----------|------------|
|                   |                 | Gene         | Protein                                  | Exponential phase                    |            |          |           |           | Stationary phase |           |          |           |            |
|                   |                 |              |  | 10°C                                 | 20°C       | 30°C     | 37°C      | 42°C E    | 10°C             | 20°C      | 30°C     | 37°C      | 42°C       |
| 1                 | 16803973        | <i>hup</i>   | DNA-binding protein HU                   | 1399 ± 4                             | 392 ± 346  | 687 ± 4  | 2259 ± 57 | 2267 ± 50 | 1410 ± 109       | 932 ± 3   | 716 ± 27 | 1136 ± 54 | 1687 ± 770 |
| 2                 | 16804055        | <i>cspB</i>  | cold-shock protein                       | 0 ± 0                                | 0 ± 0      | 18 ± 0   | 1350 ± 33 | 1429 ± 40 | 484 ± 207        | 87 ± 21   | 112 ± 26 | 444 ± 26  | 846 ± 864  |
| 3                 | 16804108        | <i>groES</i> | co-chaperonin GroES                      | 8 ± 2                                | 40 ± 26    | 39 ± 1   | 822 ± 92  | 983 ± 19  | 47 ± 5           | 47 ± 3    | 48 ± 4   | 303 ± 17  | 700 ± 419  |
| 4                 | 16803042        | <i>ptsH</i>  | phosphocarrier protein HPr               | 385 ± 32                             | 565 ± 185  | 251 ± 5  | 569 ± 18  | 589 ± 24  | 232 ± 9          | 238 ± 19  | 214 ± 18 | 232 ± 8   | 417 ± 267  |
| 5                 | 16804107        | <i>groEL</i> | molecular chaperone GroEL                | 8 ± 2                                | 34 ± 5     | 59 ± 4   | 222 ± 7   | 353 ± 21  | 119 ± 27         | 77 ± 18   | 69 ± 14  | 375 ± 9   | 384 ± 22   |
| 6                 | 16802243        |              | regulatory protein SpoVG                 | 147 ± 2                              | 264 ± 110  | 172 ± 28 | 179 ± 8   | 152 ± 3   | 208 ± 25         | 241 ± 2   | 236 ± 6  | 275 ± 6   | 215 ± 86   |
| 7                 | 16804497        | <i>gapdh</i> | glyceraldehyde-3-phosphate dehydrogenase | 152 ± 1                              | 216 ± 123  | 454 ± 13 | 148 ± 1   | 151 ± 7   | 258 ± 6          | 348 ± 10  | 278 ± 15 | 258 ± 10  | 188 ± 60   |
| 8                 | 16804690        | <i>tuf</i>   | elongation factor Tu                     | 76 ± 4                               | 295 ± 182  | 539 ± 18 | 116 ± 6   | 124 ± 5   | 161 ± 20         | 314 ± 11  | 678 ± 14 | 520 ± 45  | 275 ± 208  |
| 9                 | 16804493        | <i>eno</i>   | phosphopyruvate hydratase                | 142 ± 1                              | 326 ± 24   | 323 ± 19 | 110 ± 4   | 103 ± 7   | 232 ± 13         | 282 ± 0   | 209 ± 21 | 160 ± 9   | 130 ± 45   |
| 10                | 16803068        |              | hypothetical protein lmo1008             | 47 ± 15                              | 73 ± 30    | 55 ± 1   | 93 ± 10   | 78 ± 9    | 41 ± 1           | 65 ± 3    | 45 ± 1   | 97 ± 1    | 94 ± 14    |
| 11                | 16803697        | <i>tsf</i>   | elongation factor Ts                     | 34 ± 2                               | 64 ± 3     | 74 ± 2   | 70 ± 4    | 71 ± 1    | 52 ± 7           | 84 ± 1    | 74 ± 3   | 106 ± 16  | 100 ± 42   |
| 12                | 16803404        | <i>csp</i>   | cold-shock protein                       | 3755 ± 139                           | 1199 ± 289 | 166 ± 10 | 58 ± 19   | 79 ± 3    | 1772 ± 14        | 982 ± 102 | 424 ± 3  | 0 ± 0     | 0 ± 0      |
| 13                | 16804594        | <i>fbaA</i>  | fructose-1,6-bisphosphate aldolase       | 54 ± 5                               | 88 ± 4     | 87 ± 4   | 50 ± 1    | 47 ± 1    | 88 ± 3           | 109 ± 7   | 61 ± 0   | 129 ± 2   | 82 ± 49    |
| 14                | 16803048        |              | hypothetical protein lmo1008             | 19 ± 5                               | 0 ± 0      | 15 ± 0   | 45 ± 2    | 24 ± 3    | 28 ± 4           | 32 ± 6    | 17 ± 0   | 82 ± 0    | 47 ± 35    |
| 15                | 16803513        | <i>dnaK</i>  | molecular chaperone DnaK                 | 18 ± 3                               | 39 ± 5     | 44 ± 0   | 44 ± 2    | 44 ± 2    | 27 ± 1           | 41 ± 2    | 50 ± 2   | 106 ± 0   | 86 ± 61    |
| 16                | 16803354        |              | ribosome recycling factor                | 36 ± 0                               | 6 ± 2      | 6 ± 0    | 42 ± 3    | 31 ± 3    | 34 ± 3           | 49 ± 2    | 0 ± 0    | 56 ± 1    | 49 ± 29    |
| 17                | 16804496        | <i>pgk</i>   | phosphoglycerate kinase                  | 30 ± 1                               | 70 ± 14    | 89 ± 5   | 42 ± 2    | 42 ± 4    | 53 ± 3           | 73 ± 7    | 67 ± 2   | 74 ± 0    | 65 ± 28    |
| 18                | 16804262        |              | hypothetical observed protein lmo2223    | 38 ± 4                               | 45 ± 3     | 87 ± 9   | 39 ± 1    | 31 ± 5    | 21 ± 1           | 80 ± 3    | 58 ± 5   | 65 ± 8    | 54 ± 28    |
| 19                | 16802983        | <i>fri</i>   | non-heme iron-binding ferritin           | 31 ± 4                               | 37 ± 6     | 69 ± 4   | 36 ± 5    | 34 ± 1    | 53 ± 6           | 83 ± 4    | 106 ± 17 | 63 ± 8    | 52 ± 27    |
| 20                | 16802242        |              | regulatory protein SpoVG                 | 24 ± 0                               | 36 ± 11    | 22 ± 0   | 34 ± 4    | 28 ± 2    | 22 ± 3           | 23 ± 1    | 24 ± 0   | 42 ± 13   | 33 ± 8     |

Rank<sup>a</sup> was calculated based on the expression at the exponential phase of 37°C cultivation.

GI<sup>b</sup>: gene accession number (pubmed)

**Supplementary Table 3.** The summary of cell growth-related protein expressions

| GI                           | Gene        | Product                                    | Exponential |             |            |            |            | Stationary |             |            |            |            |
|------------------------------|-------------|--|-------------|-------------|------------|------------|------------|------------|-------------|------------|------------|------------|
|                              |             |  | 10°C        | 20°C        | 30°C       | 37°C       | 42°C       | 10°C       | 20°C        | 30°C       | 37°C       | 42°C       |
| <b>ATP synthase</b>          |             |  |             |             |            |            |            |            |             |            |            |            |
| 16804569                     | <i>atpA</i> | ATP synthase F0F1 subunit epsilon          | 9.8 ± 0.0   | 25.5 ± 11.5 | 26.7 ± 0.3 | 10.2 ± 0.2 | 9.0 ± 0.0  | 27.1 ± 4.4 | 26.6 ± 6.6  | 20.4 ± 0.7 | 25.6 ± 2.2 | 20.9 ± 3.0 |
| 16804566                     | <i>atpC</i> | ATP synthase F0F1 subunit beta             | 4.6 ± 0.0   | 0.0         | 4.4 ± 0.1  | 4.8 ± 0.1  | 2.2        | 7.8        | 3.9         |            | 7.8        | 3.9        |
| 16804567                     | <i>atpD</i> | ATP synthase F0F1 subunit alpha            | 18.7 ± 3.3  | 44.7 ± 3.6  | 53.2 ± 4.2 | 13.9 ± 0.8 | 13.8 ± 1.3 | 46.8 ± 6.3 | 45.7 ± 0.0  | 45.7 ± 3.2 | 38.4 ± 2.4 | 35.7 ± 4.7 |
| 16804571                     | <i>atpF</i> | ATP synthase F0F1 subunit delta            | 1.7         | 0.0         | 10.1 ± 0.2 | 0.0        | 0.0        | 4.4 ± 2.1  | 5.9 ± 0.0   |            | 3.0        | 3.0        |
| 16804570                     | <i>atpH</i> | ATP synthase F0F1 subunit B                | 10.8 ± 1.1  | 10.4        | 8.1 ± 2.5  | 10.4 ± 0.2 | 6.5 ± 2.3  | 17.0 ± 0.0 | 11.3 ± 4.0  | 5.7 ± 0.0  | 8.5 ± 4.0  | 11.3 ± 4.0 |
| <b>Aminos acid synthesis</b> |             |  |             |             |            |            |            |            |             |            |            |            |
| 16803018                     |             | branched-chain amino acid aminotransferase | 7.7 ± 3.2   | 10.7 ± 7.1  | 13.1 ± 1.0 | 7.0 ± 0.8  | 5.3 ± 1.2  | 12.3 ± 2.2 | 13.1 ± 1.1  | 10.8 ± 2.2 | 22.3 ± 1.1 | 28.4 ± 3.3 |
| 16802269                     | <i>cysK</i> | cysteine synthase                          | 11.0 ± 0.8  | 16.6 ± 2.1  | 18.3 ± 0.4 | 20.7 ± 1.1 | 19.5 ± 1.5 | 20.5 ± 1.3 | 22.3 ± 1.3  | 18.8 ± 3.8 | 30.4 ± 5.1 | 33.9 ± 0.0 |
| 16802896                     | <i>ddl</i>  | D-alanyl-alanine synthetase A              | 0.0         | 5.0 ± 0.3   | 1.6        | 0.0        | 0.0        |            | 4.2 ± 2.0   | 2.8        | 5.0 ± 1.0  | 7.8 ± 1.0  |
| 16803475                     | <i>dapA</i> | dihydrodipicolinate synthase               | 0.0         | 24.8 ± 8.8  | 31.2 ± 2.3 | 19.0 ± 2.8 | 18.4 ± 3.7 | 11.0 ± 0.0 | 25.6 ± 15.5 | 11.0 ± 5.2 | 24.7 ± 3.9 | 24.7 ± 1.3 |
| 16803659                     |             | D-amino acid aminotransferase              | 3.1         | 6.0         | 4.0        | 2.2        | 1.0        | 7.1        | 8.9 ± 2.5   | 1.8 ± 0.0  | 3.5        | 4.4 ± 1.3  |
| 16803704                     | <i>metK</i> | metadenosylmethionine synthetase           | 0.8 ± 0.0   | 1.7 ± 0.7   | 2.2 ± 1.0  | 0.8 ± 0.0  | 0.0        | 1.3        | 1.3 ± 0.0   | 2.0 ± 0.9  | 3.3 ± 0.9  | 2.0 ± 0.9  |
| <b>Cell Growth</b>           |             |  |             |             |            |            |            |            |             |            |            |            |
| 16804072                     | <i>ftsA</i> | cell division protein FtsA                 | 0.7         | 1.2         | 5.7 ± 1.9  | 0.0        | 0.0        | 1.3        | 3.8 ± 1.8   | 6.3        | 6.3 ± 1.8  | 4.4 ± 0.9  |
| 16803811                     | <i>ftsA</i> | cell division protein FtsA                 | 3.6         | 0.0         | 0.0        | 0.0        | 0.0        |            |             |            |            |            |
| 16804071                     | <i>ftsZ</i> | cell division protein FtsZ                 | 18.4 ± 1.7  | 27.0 ± 1.9  | 23.0 ± 6.1 | 18.7 ± 2.8 | 14.0 ± 2.8 | 37.6 ± 0.0 | 37.6 ± 3.9  | 22.3 ± 5.9 | 29.9 ± 6.9 | 31.3 ± 3.0 |
| 16804563                     | <i>mbl</i>  | rod shape-determining protein MreB         | 1.0         | 15.9 ± 7.0  | 19.3 ± 4.3 | 2.5 ± 0.7  | 2.3 ± 0.7  | 7.3 ± 1.1  | 16.2 ± 2.3  | 23.4 ± 3.4 | 14.5 ± 0.0 | 11.3 ± 0.0 |
| 16803588                     | <i>mreB</i> | rod shape-determining protein MreB         | 18.1 ± 2.6  | 33.5 ± 20.2 | 41.4 ± 3.0 | 10.9 ± 1.2 | 10.2 ± 0.0 | 32.4 ± 2.3 | 34.8 ± 3.4  | 38.9 ± 0.0 | 21.9 ± 3.4 | 17.0 ± 1.1 |
| 16802266                     | <i>ftsH</i> | cell division protein FtsH                 | 1.3 ± 0.0   | 3.7 ± 0.3   | 5.6 ± 0.5  | 0.5        | 0.2        | 1.9 ± 0.5  | 3.0 ± 1.1   | 5.7 ± 0.5  | 3.4 ± 0.5  | 2.6 ± 0.5  |
| 16803843                     | <i>ftsY</i> | cell division protein FtsY [               | 0.0         | 0.0         | 5.5        | 0.0        | 0.0        |            |             | 1.6        | 1.6        |            |
| 16804827                     | <i>parB</i> | partition protein ParB homolog             | 0.0         | 0.0         | 0          | 1.6 ± 0.7  | 1.5 ± 0.7  |            | 2.7 ± 1.3   | 3.6        | 5.4 ± 0.0  | 4.5 ± 1.3  |
| <b>Lipid metabolism</b>      |             |  |             |             |            |            |            |            |             |            |            |            |
| 16803847                     | <i>fabG</i> | 3-ketoacyl-ACP reductase                   | 12.3 ± 2.8  | 34.1 ± 6.1  | 30.0 ± 4.2 | 14.7 ± 1.6 | 10.7 ± 4.4 | 15.4 ± 0.0 | 16.5 ± 1.6  | 30.7 ± 3.1 | 14.3 ± 4.7 | 13.2 ± 3.1 |
| 16804240                     |             | 3-oxoacyl-ACP synthase                     | 2.7 ± 0.5   | 11.5 ± 0.7  | 11.1 ± 0.8 | 3.9 ± 1.0  | 3.0 ± 1.0  | 3.9 ± 0.0  | 5.8 ± 2.8   | 12.3 ± 2.8 | 6.5 ± 0.0  | 5.2 ± 3.7  |
| 16802828                     |             | ACP phosphodiesterase                      | 7.3 ± 0.0   | 22.2 ± 7.5  | 11.3 ± 0.2 | 3.8 ± 1.0  | 3.6 ± 1.0  | 5.0        | 18.7 ± 5.3  | 10.0 ± 3.5 | 5.0        | 7.5 ± 0.0  |
| 16803848                     | <i>fabD</i> | ACP S-malonyltransferase                   | 3.6 ± 2.2   | 3.9 ± 1.3   | 5.0 ± 1.3  | 3.7 ± 0.7  | 2.0        | 6.1 ± 1.2  | 4.4 ± 3.7   | 3.5        | 3.5 ± 0.0  | 7.9 ± 6.2  |
| 16803010                     |             | enoyl-ACP reductase                        | 1.2         | 17.8 ± 4.0  | 18.5 ± 2.9 | 2.5 ± 0.0  | 2.3 ± 0.0  | 5.1 ± 1.4  | 8.1 ± 2.9   | 12.2 ± 0.0 | 8.1 ± 0.0  | 7.1 ± 1.4  |
| 16802399                     |             | fatty-acid--CoA ligase                     | 0.0         | 1.8 ± 0.1   | 5.1 ± 0.7  | 0.0        | 0.0        | 2.0        | 2.5 ± 0.7   | 2.5 ± 0.7  |            | 2.0 ± 1.4  |

**Supplementary Table 4.** The summary of heat shock and stress response protein expressions

| GI       | Gene         | Product                   | Exponential    |                |             |               |               | Stationary    |              |             |              |              |
|----------|--------------|---------------------------|----------------|----------------|-------------|---------------|---------------|---------------|--------------|-------------|--------------|--------------|
|          |              |                           | 10°C           | 20°C           | 30°C        | 37°C          | 42°C          | 10°C          | 20°C         | 30°C        | 37°C         | 42°C         |
| 16803513 | <i>dnaK</i>  | molecular chaperone DnaK  | 17.6 ± 3.3     | 39.0 ± 5.3     | 44.0 ± 0.3  | 43.8 ± 2.0    | 43.7 ± 2.3    | 27.4 ± 1.8    | 36.5 ± 0.0   | 38.7 ± 0.6  | 83.5 ± 1.2   | 98.7 ± 6.8   |
| 16804107 | <i>groEL</i> | molecular chaperone GroEL | 8.0 ± 2.1      | 34.3 ± 5.2     | 58.8 ± 3.7  | 222.1 ± 6.9   | 353.3 ± 21.0  | 122.4 ± 31.2  | 69.7 ± 19.2  | 52.7 ± 9.2  | 296.5 ± 3.5  | 311.6 ± 13.5 |
| 16804108 | <i>groES</i> | co-chaperonin GroES       | 8.4 ± 2.4      | 39.5 ± 26.1    | 38.9 ± 0.8  | 822.1 ± 91.8  | 983.4 ± 19.1  | 48.4 ± 4.0    | 42.7 ± 4.0   | 37.0 ± 4.0  | 239.1 ± 16.1 | 287.5 ± 52.3 |
| 16804055 | <i>cspB</i>  | cold-shock protein        | 0.0            | 0.0            | 18.2        | 1350.4 ± 33.4 | 1428.6 ± 39.5 | 500.2 ± 228.4 | 78.8 ± 22.3  | 86.6 ± 22.3 | 350.5 ± 16.7 | 193.0 ± 5.6  |
| 16803404 | <i>cspL</i>  | cold-shock protein        | 3755.0 ± 139.2 | 1198.7 ± 288.5 | 165.8 ± 9.9 | 57.5 ± 19.3   | 79.2 ± 3.4    | 1819.6 ± 44.6 | 882.2 ± 55.7 | 326.9 ± 5.6 |              |              |
| 16802268 | <i>hslO</i>  | heat shock protein 33     | 0.0            | 1.7            | 0.0         | 0.0           | 0.0           |               |              |             |              | 3.6          |
| 16803514 | <i>grpE</i>  | heat shock protein GrpE   | 3.1            | 9.7            | 13.5 ± 6.6  | 14.4 ± 0.3    | 18.1 ± 0.1    | 7.9 ± 0.0     | 11.8 ± 1.9   | 10.5        | 21.0 ± 0.0   | 23.6 ± 0.0   |
| 16804258 |              | foldase                   | 7.2 ± 0.0      | 27.6 ± 11.6    | 11.0 ± 1.7  | 0.0           | 0.0           | 16.7 ± 1.2    | 7.0 ± 0.0    | 12.3 ± 2.5  | 2.6 ± 1.2    |              |
| 16804822 | <i>kat</i>   | catalase                  | 6.9 ± 1.3      | 38.9 ± 6.7     | 59.0 ± 9.5  | 6.3 ± 1.9     | 5.3 ± 0.0     | 17.5 ± 1.5    | 46.8 ± 0.7   | 42.2 ± 5.8  | 34.5 ± 2.2   | 20.1 ± 2.2   |
| 16803479 | <i>sod</i>   | superoxide dismutase      | 28.4 ± 0.1     | 30.2 ± 6.2     | 33.3 ± 2.8  | 32.6 ± 5.0    | 33.6 ± 2.0    | 44.5 ± 1.8    | 62.3 ± 1.8   | 33.1 ± 0.0  | 52.2 ± 1.8   | 49.6 ± 12.6  |
| 16803641 |              | general stress protein    | 5.5 ± 2.6      | 20.5 ± 8.6     | 16.0 ± 2.2  | 10.4 ± 3.8    | 9.0 ± 2.6     | 12.5 ± 0.0    | 17.2 ± 2.2   | 14.1 ± 2.2  | 15.6 ± 8.8   | 18.8 ± 0.0   |
| 16804407 |              | general stress protein 13 | 6.5 ± 1.8      | 5.8 ± 2.4      | 0.0         | 10.8 ± 0.2    | 14.0 ± 1.8    | 6.6 ± 3.1     |              |             |              |              |

**Supplementary Table 5.** The summary of the central carbon catabolic enzymes expressions

| GI                  | Gene | Product                                  | Exponential |               |              |             |             | Stationary  |              |              |              |             |
|---------------------|------|--|-------------|---------------|--------------|-------------|-------------|-------------|--------------|--------------|--------------|-------------|
|                     |      |  | 10°C        | 20°C          | 30°C         | 37°C        | 42°C        | 10°C        | 20°C         | 30°C         | 37°C         | 42°C        |
| <b>Glycolysis</b>   |      |  |             |               |              |             |             |             |              |              |              |             |
| 16803379            | gck  | glucose kinase                           | 4.5 ± 0.7   | 18.7 ± 6.4    | 11.6 ± 0.3   | 3.6 ± 0.7   | 2.5 ± 0.7   | 6.8 ± 0.0   | 11.9 ± 2.4   | 12.8 ± 1.2   | 8.5 ± 0.0    | 9.4 ± 3.6   |
| 16804405            | pgi  | glucose-6-phosphate isomerase            | 7.4 ± 0.9   | 9.9 ± 8.5     | 28.2 ± 3.4   | 7.4 ± 0.6   | 4.6 ± 0.9   | 15.6 ± 4.1  | 13.3 ± 0.8   | 10.9 ± 0.8   | 10.4 ± 1.6   | 14.4 ± 0.8  |
| 16803611            | pfkA | 6-phosphofructokinase                    | 14.7 ± 0.1  | 51.7 ± 23.1   | 52.3 ± 0.2   | 28.5 ± 0.9  | 24.0 ± 5.4  | 28.4 ± 0.0  | 44.3 ± 8.3   | 41.8 ± 2.4   | 55.2 ± 2.4   | 49.3 ± 3.5  |
| 16804594            | fbaA | fructose-1,6-bisphosphate aldolase       | 54.1 ± 5.0  | 87.9 ± 4.4    | 87.1 ± 4.3   | 50.3 ± 1.0  | 46.8 ± 0.9  | 90.1 ± 0.0  | 97.8 ± 2.7   | 47.0 ± 1.4   | 101.6 ± 0.0  | 93.9 ± 0.0  |
| 16804495            | tpiA | triosephosphate isomerase                | 32.0 ± 2.8  | 63.6 ± 13.1   | 70.4 ± 5.3   | 33.2 ± 0.3  | 33.8 ± 2.5  | 48.1 ± 4.5  | 49.2 ± 9.1   | 51.3 ± 6.0   | 54.5 ± 7.6   | 54.5 ± 1.5  |
| 16804497            | gap  | glyceraldehyde-3-phosphate dehydrogenase | 151.7 ± 0.7 | 215.6 ± 122.5 | 453.8 ± 13.1 | 147.8 ± 1.2 | 151.1 ± 7.3 | 264.5 ± 2.2 | 312.9 ± 3.4  | 213.9 ± 6.7  | 203.6 ± 10.1 | 190.1 ± 6.7 |
| 16804496            | pgk  | phosphoglycerate kinase                  | 30.1 ± 0.5  | 69.8 ± 13.5   | 88.5 ± 4.7   | 41.6 ± 1.5  | 42.0 ± 4.0  | 54.0 ± 4.8  | 66.2 ± 8.7   | 51.9 ± 0.0   | 58.0 ± 1.0   | 64.2 ± 5.8  |
| 16804494            | pgm  | phosphoglyceromutase                     | 10.5 ± 2.2  | 21.2 ± 1.9    | 25.7 ± 2.2   | 13.4 ± 0.7  | 11.5 ± 1.2  | 18.5 ± 1.4  | 21.5 ± 1.4   | 19.0 ± 0.7   | 27.7 ± 1.4   | 24.1 ± 0.7  |
| 16804493            | eno  | phosphopyruvate hydratase                | 142.3 ± 1.1 | 325.5 ± 24.2  | 322.9 ± 19.0 | 109.6 ± 4.3 | 102.6 ± 6.7 | 237.9 ± 5.3 | 254.1 ± 10.5 | 161.1 ± 12.3 | 126.4 ± 5.3  | 128.3 ± 2.6 |
| 16803610            | pykA | pyruvate kinase                          | 25.1 ± 2.0  | 69.3 ± 25.3   | 73.6 ± 2.1   | 13.2 ± 0.1  | 11.6 ± 0.7  | 41.3 ± 3.9  | 50.1 ± 4.5   | 36.3 ± 1.9   | 32.2 ± 2.6   | 31.7 ± 0.6  |
| 16803092            | pdhA | pyruvate dehydrogenase subunit E1 alpha  | 6.6 ± 1.2   | 20.4 ± 2.1    | 25.4 ± 1.7   | 5.5 ± 0.7   | 6.0 ± 0.6   | 15.4 ± 2.0  | 27.2 ± 1.0   | 29.3 ± 2.0   | 13.3 ± 1.0   | 20.2 ± 1.0  |
| 16803093            | pdhB | pyruvate dehydrogenase subunit E1 beta   | 2.9 ± 1.4   | 21.7 ± 3.3    | 15.8 ± 1.7   | 5.0 ± 1.3   | 4.7 ± 0.0   | 10.6 ± 1.2  | 21.2 ± 2.3   | 35.0 ± 1.2   | 10.6 ± 1.2   | 11.4 ± 0.0  |
| 16803094            | pdhC | dihydrolipoamide acetyltransferase E2    | 2.3 ± 0.8   | 8.0 ± 4.2     | 11.8 ± 2.1   | 3.3 ± 1.3   | 2.8         | 11.9 ± 1.4  | 16.3 ± 4.9   | 14.8 ± 1.4   | 9.9 ± 1.4    | 6.9 ± 1.4   |
| 16803095            | pdhD | dihydrolipoamide dehydrogenase E3        | 3.4 ± 0.0   | 10.7 ± 1.5    | 11.9 ± 2.1   | 1.4 ± 0.0   | 0.7         | 13.4 ± 0.8  | 16.3 ± 1.6   | 12.8 ± 0.0   | 3.5 ± 0.0    | 2.3 ± 0.0   |
| <b>Fermentation</b> |      |  |             |               |              |             |             |             |              |              |              |             |
| 16802256            | ldh  | L-lactate dehydrogenase                  | 1.0 ± 0.0   | 6.5 ± 7.0     | 15.2 ± 5.1   | 3.6 ± 0.8   | 4.3 ± 0.7   | 4.2 ± 1.2   | 10.1 ± 2.4   | 4.2 ± 1.2    | 9.2 ± 3.6    | 8.4 ± 2.4   |
| 16803956            | pflA | pyruvate formate-lyase                   | 16.0 ± 2.5  | 26.8 ± 0.7    | 27.9 ± 1.0   | 1.7         | 0.4         | 32.6 ± 4.3  | 21.5 ± 5.7   | 20.5 ± 0.5   | 5.4 ± 1.9    | 2.0 ± 1.0   |
| 16803446            | pflB | pyruvate formate-lyase                   | 12.7 ± 1.9  | 35.3 ± 6.1    | 32.8 ± 1.5   | 0.4         | 0.0         | 31.9 ± 1.5  | 35.0 ± 1.0   | 26.8 ± 0.0   | 7.9 ± 0.5    | 10.3 ± 2.9  |
| 16803674            | adh  | acetaldehyde-CoA/alcohol dehydrogenase   | 41.5        | 70.1 ± 16.0   | 58.4 ± 1.2   | 8.2 ± 1.2   | 5.8 ± 0.2   | 77.2 ± 2.6  | 61.7 ± 1.3   | 35.6 ± 2.1   | 33.4 ± 3.4   | 34.6 ± 0.9  |
| 16804142            | pta  | phosphotransacetylase                    | 9.3 ± 0.7   | 21.6          | 22.8 ± 3.2   | 11.7 ± 1.0  | 10.1 ± 0.7  | 16.7 ± 2.4  | 20.1 ± 0.0   | 15.9 ± 1.2   | 12.5 ± 1.2   | 13.4 ± 2.4  |
| 16803621            | ackA | acetate kinase                           | 13.1 ± 1.1  | 26.5 ± 6.6    | 30.6 ± 0.4   | 5.6 ± 0.1   | 2.6 ± 0.5   | 30.2 ± 1.9  | 28.9 ± 1.9   | 23.0 ± 0.9   | 15.1 ± 0.9   | 11.2 ± 2.8  |
| <b>TCA</b>          |      |  |             |               |              |             |             |             |              |              |              |             |
| 16803112            | pycA | pyruvate carboxylase                     | 0.7 ± 0.2   | 1.4 ± 0.2     | 3.3 ± 0.4    | 0.0         | 0.0         | 1.3 ± 0.6   | 2.0 ± 0.3    | 1.3 ± 0.0    | 1.8 ± 0.6    | 2.0 ± 0.3   |
| 16803681            | citB | aconitate hydratase                      | 0.0         | 2.1 ± 0.1     | 0.7 ± 0.0    | 0.0         | 0.0         |             | 0.6 ± 0.0    |              | 1.2          | 0.9 ± 0.4   |
| 16802400            | fum  | fumarate reductase subunit A             | 3.7 ± 1.8   | 26.0 ± 6.4    | 57.0 ± 11.5  | 7.7 ± 1.1   | 8.8 ± 0.5   | 4.8 ± 0.7   | 10.6 ± 3.0   | 34.4 ± 2.2   | 11.1 ± 2.2   | 11.1 ± 2.2  |



**PPP**

|                     |      |  |            |            |            |           |           |            |            |            |           |           |
|---------------------|------|--|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|
| 16804017            |      | glucose-6-phosphate 1-dehydrogenase                | 0.0        | 2.7 ± 1.1  | 3.5        | 0.0       | 0.0       |            |            |            |           |           |
| 16803416            |      | 6-phosphogluconate dehydrogenase                   | 12.6 ± 0.4 | 24.7 ± 0.8 | 26.8 ± 2.1 | 1.7 ± 0.5 | 0.6       | 20.3 ± 2.3 | 15.9 ± 0.8 | 13.7 ± 3.9 | 6.0 ± 0.8 | 3.3 ± 1.6 |
| 16803993            | drm  | phosphopentomutase                                 | 6.2 ± 1.1  | 8.2 ± 2.1  | 12.7 ± 0.8 | 4.8 ± 1.2 | 2.6 ± 0.5 | 14.5 ± 1.9 | 11.8 ± 0.0 | 9.2 ± 1.9  | 8.6 ± 2.8 | 7.2 ± 0.9 |
| 16803345            | tkt  | transketolase                                      | 2.8 ± 0.0  | 8.0 ± 4.0  | 11.8 ± 0.3 | 1.5       | 1.8 ± 0.6 | 8.0 ± 1.1  | 7.2 ± 1.1  | 3.6 ± 0.6  | 5.6 ± 2.3 | 6.8 ± 0.6 |
| Amino sugar/UDP-Hex |      |  |            |            |            |           |           |            |            |            |           |           |
| 16802769            | glmS | glucosamine--fructose-6-phosphate aminotransferase | 1.0        | 1.6        | 6.0 ± 1.3  | 0.0       | 0.5       | 2.6 ± 0.0  | 2.6 ± 0.0  | 3.9 ± 0.6  | 7.4 ± 0.6 | 6.1 ± 2.5 |
| 16804157            | glmM | phosphoglucosamine mutase                          | 3.1 ± 0.5  | 7.4 ± 1.9  | 6.7 ± 0.1  | 1.8 ± 1.5 | 2.0       | 4.7 ± 0.0  | 4.7 ± 0.0  | 4.7 ± 1.7  | 8.3 ± 1.7 | 7.7 ± 0.8 |
| 16804149            |      | mannose-6-phosphate isomerase                      | 1.4 ± 0.7  | 1.5        | 1.9 ± 0.0  | 1.5 ± 0.7 | 1.9 ± 0.0 | 1.6 ± 0.0  | 1.6 ± 0.0  | 1.6        | 3.3 ± 2.3 | 3.3 ± 0.0 |
| 16804513            |      | phosphoglucomutase                                 | 1.1        | 3.9 ± 0.9  | 3.6 ± 2.2  | 0.0       | 0.0       | 2.2 ± 0.6  |            |            | 3.1 ± 0.6 | 2.7 ± 1.3 |
| <b>Etc.</b>         |      |  |            |            |            |           |           |            |            |            |           |           |
| 16803127            |      | glucitol dehydrogenase                             | 3.1 ± 0.6  | 4.1        | 9.3 ± 3.4  | 1.8       | 0.9 ± 0.0 | 5.2 ± 1.1  | 4.5 ± 0.0  | 7.5 ± 0.0  | 6.0 ± 0.0 | 6.7 ± 1.1 |
| 16802237            |      | phospho-beta-glucosidase                           | 4.9 ± 0.0  | 8.4 ± 1.8  | 8.4 ± 1.9  | 3.9 ± 1.9 | 4.2 ± 0.9 | 6.3 ± 0.0  | 5.3 ± 1.5  | 3.2 ± 1.5  | 3.2 ± 1.5 | 5.3 ± 4.5 |
| 16802582            |      | tagatose 1,6-diphosphate aldolase                  | 2.2 ± 1.9  | 4.0 ± 1.7  | 5.2 ± 2.6  | 2.3 ± 1.9 | 1.8 ± 0.0 | 6.1 ± 4.3  | 4.6 ± 4.3  | 1.5 ± 0.0  | 2.3 ± 1.1 | 4.6 ± 0.0 |
| 16804034            |      | deoxyribose-phosphate aldolase                     | 0.0        | 0.0        | 5.5        | 0.0       | 1.4 ± 0.0 |            |            |            |           |           |

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**Supplementary Table 6.** The summary of protein synthesis-related protein expressions

| GI                       | Gene        | Product                      | Exponential  |               |             |              |              | Stationary    |              |              |             |              |
|--------------------------|-------------|------------------------------|--------------|---------------|-------------|--------------|--------------|---------------|--------------|--------------|-------------|--------------|
|                          |             |                              | 10°C         | 20°C          | 30°C        | 37°C         | 42°C         | 10°C          | 20°C         | 30°C         | 37°C        | 42°C         |
| <b>Ribosomal Protein</b> |             |                              |              |               |             |              |              |               |              |              |             |              |
| 16803977                 | <i>rpsA</i> | 30S ribosomal protein S1     | 2.4 ± 1.1    | 5.5 ± 2.3     | 7.9 ± 0.2   | 7.2 ± 0.5    | 3.6 ± 0.6    | 9.7 ± 3.9     | 9.7 ± 0.0    | 6.3 ± 2.9    | 15.3 ± 3.9  | 11.8 ± 1.0   |
| 16803698                 | <i>rpsB</i> | 30S ribosomal protein S2     | 35.1 ± 1.0   | 182.8 ± 76.5  | 110.5 ± 2.4 | 45.1 ± 1.7   | 44.2 ± 0.1   | 63.8 ± 12.9   | 98.2 ± 1.4   | 103.3 ± 14.3 | 79.0 ± 5.7  | 73.9 ± 7.2   |
| 16804664                 | <i>rpsC</i> | 30S ribosomal protein S3     | 13.8 ± 1.9   | 21.5 ± 9.0    | 23.9 ± 7.0  | 20.8 ± 0.6   | 16.2 ± 3.8   | 18.8 ± 0.0    | 31.7 ± 1.7   | 25.8 ± 0.0   | 31.7 ± 1.7  | 29.3 ± 1.7   |
| 16803636                 | <i>rpsD</i> | 30S ribosomal protein S4     | 3.0          | 19.5 ± 15.4   | 31.6 ± 3.4  | 7.7 ± 2.3    | 7.3 ± 4.1    | 10.1 ± 3.6    | 17.7 ± 3.6   | 19.0 ± 1.8   | 15.2 ± 3.6  | 13.9 ± 1.8   |
| 16804653                 | <i>rpsE</i> | 30S ribosomal protein S5     | 19.4 ± 8.2   | 56.0 ± 31.8   | 11.4        | 27.2 ± 3.7   | 23.7 ± 1.3   | 14.9 ± 2.3    | 14.9 ± 2.3   | 19.8 ± 0.0   | 5.0 ± 2.3   | 6.6 ± 0.0    |
| 16802092                 | <i>rpsF</i> | 30S ribosomal protein S6     | 83.7 ± 6.6   | 82.8 ± 38.8   | 39.8 ± 0.9  | 131.0 ± 14.7 | 90.5 ± 1.8   | 50.0 ± 0.0    | 50.0 ± 0.0   | 35.0 ± 7.1   | 47.5 ± 10.6 | 72.5 ± 10.6  |
| 16804692                 | <i>rpsG</i> | 30S ribosomal protein S7     | 55.0 ± 2.5   | 38.1 ± 15.9   | 44.1 ± 1.0  | 54.2 ± 3.1   | 39.0 ± 2.5   | 58.1 ± 18.3   | 61.4 ± 9.1   | 9.7 ± 0.0    | 50.1 ± 2.3  | 63.0 ± 6.9   |
| 16804656                 | <i>rpsH</i> | 30S ribosomal protein S8     | 46.3 ± 3.1   | 22.7 ± 3.8    | 17.9 ± 5.9  | 52.9 ± 7.8   | 34.0 ± 0.1   | 23.6 ± 0.0    | 23.6 ± 5.6   | 17.7 ± 2.8   | 25.6 ± 2.8  | 27.6 ± 0.0   |
| 16804634                 | <i>rpsI</i> | 30S ribosomal protein S9     | 35.2 ± 0.1   | 18.4          | 47.7 ± 2.2  | 40.2 ± 0.9   | 33.3 ± 1.5   | 33.9 ± 2.8    | 37.9 ± 2.8   | 20.0 ± 0.0   | 31.9 ± 0.0  | 41.9 ± 8.5   |
| 16804671                 | <i>rpsJ</i> | 30S ribosomal protein S10    | 109.7 ± 8.6  | 120.0 ± 54.3  | 103.5 ± 6.2 | 100.5 ± 12.6 | 87.6 ± 0.3   | 108.1 ± 7.0   | 86.0 ± 10.4  | 88.5 ± 20.9  | 90.9 ± 10.4 | 100.8 ± 17.4 |
| 16804645                 | <i>rpsK</i> | 30S ribosomal protein S11    | 58.8 ± 3.7   | 112.9 ± 40.2  | 113.8 ± 9.2 | 87.6 ± 3.7   | 69.5 ± 3.2   | 75.0 ± 11.8   | 97.9 ± 2.9   | 81.3 ± 8.8   | 79.2 ± 5.9  | 85.4 ± 14.7  |
| 16803370                 | <i>rpsO</i> | 30S ribosomal protein S15    | 3.2 ± 0.0    | 9.2           | 9.3 ± 4.6   | 6.6 ± 0.1    | 4.7 ± 2.2    |               |              |              | 5.4         |              |
| 16803837                 | <i>rpsP</i> | 30S ribosomal protein S16    | 19.5 ± 0.1   | 31.5 ± 8.5    | 22.0 ± 4.0  | 20.2 ± 0.4   | 19.1 ± 4.6   | 33.2 ± 0.0    | 22.1 ± 0.0   | 19.4 ± 3.9   | 22.1 ± 7.8  | 30.4 ± 3.9   |
| 16804661                 | <i>rpsQ</i> | 30S ribosomal protein S17    | 47.3 ± 0.2   | 37.1          | 26.2 ± 0.6  | 40.2 ± 16.6  | 74.4 ± 2.6   | 28.8 ± 0.0    | 8.6 ± 4.1    | 23.0 ± 16.3  |             |              |
| 16804666                 | <i>rpsS</i> | 30S ribosomal protein S19    | 57.9 ± 4.8   | 40.4          | 40.6 ± 14.1 | 93.5 ± 2.9   | 91.3 ± 4.7   | 54.8 ± 0.0    | 24.6 ± 3.9   | 19.2 ± 3.9   | 24.6 ± 3.9  | 24.6 ± 3.9   |
| 16802295                 | <i>rplA</i> | 50S ribosomal protein L1     | 30.3 ± 4.0   | 169.7 ± 80.9  | 80.0 ± 2.0  | 47.3 ± 3.0   | 58.0 ± 1.7   | 43.4 ± 5.0    | 70.4 ± 3.3   | 76.3 ± 1.7   | 57.5 ± 5.0  | 41.1 ± 11.6  |
| 16804667                 | <i>rplB</i> | 50S ribosomal protein L2     | 4.4 ± 1.5    | 4.9 ± 2.1     | 20.3 ± 7.1  | 0.0          | 0.0          | 4.7 ± 4.0     | 4.7 ± 1.3    | 4.7 ± 1.3    | 5.7         |              |
| 16804670                 | <i>rplC</i> | 50S ribosomal protein L3     | 25.9 ± 3.2   | 118.4 ± 10.1  | 83.2 ± 5.9  | 43.9 ± 2.0   | 50.0 ± 3.2   | 26.5 ± 1.8    | 69.4 ± 8.9   | 60.5 ± 7.1   | 41.6 ± 5.4  | 47.9 ± 10.7  |
| 16804669                 | <i>rplD</i> | 50S ribosomal protein L4     | 18.7 ± 5.4   | 97.3 ± 14.9   | 94.1 ± 8.2  | 18.7 ± 4.8   | 23.4 ± 0.1   | 38.2 ± 7.2    | 48.3 ± 7.2   | 63.6 ± 3.6   | 36.9 ± 1.8  | 34.3 ± 5.4   |
| 16804658                 | <i>rplE</i> | 50S ribosomal protein L5     | 60.8 ± 5.0   | 166.4 ± 40.5  | 135.7 ± 0.6 | 58.7 ± 2.6   | 52.1 ± 3.7   | 67.6 ± 10.2   | 96.3 ± 6.1   | 138.0 ± 20.3 | 48.9 ± 16.3 | 57.5 ± 0.0   |
| 16804655                 | <i>rplF</i> | 50S ribosomal protein L6     | 80.1 ± 2.8   | 177.3 ± 69.2  | 124.7 ± 2.1 | 81.3 ± 1.0   | 76.7 ± 4.6   | 94.9 ± 4.2    | 108.2 ± 6.3  | 111.2 ± 10.5 | 100.8 ± 8.4 | 109.7 ± 8.4  |
| 16802297                 | <i>rplL</i> | 50S ribosomal protein L7/L12 | 173.0 ± 19.8 | 602.7 ± 664.8 | 1206 ± 22.0 | 147.2 ± 15.0 | 134.9 ± 15.4 | 294.4 ± 110.6 | 524.4 ± 19.5 | 823.4 ± 13.0 | 218.5 ± 9.8 | 149.5 ± 9.8  |
| 16802101                 | <i>rplI</i> | 50S ribosomal protein L9     | 17.7 ± 1.4   | 3.3           | 20.2 ± 6.1  | 44.4 ± 0.7   | 35.7 ± 4.4   | 21.3 ± 0.0    | 16.0 ± 2.5   | 5.3 ± 2.5    | 37.3 ± 7.5  | 40.8 ± 2.5   |
| 16802296                 | <i>rplJ</i> | 50S ribosomal protein L10    | 37.2 ± 1.5   | 115.0 ± 39.9  | 57.4 ± 9.1  | 33.7 ± 3.5   | 31.7 ± 2.7   | 39.0 ± 4.6    | 40.6 ± 16.1  | 35.7 ± 4.6   | 30.9 ± 2.3  | 32.5 ± 4.6   |
| 16802294                 | <i>rplK</i> | 50S ribosomal protein L11    | 47.6 ± 0.2   | 81.8          | 85.6 ± 1.2  | 62.4 ± 2.9   | 63.2 ± 10.8  | 46.3 ± 10.9   | 69.5 ± 5.5   | 28.9 ± 2.7   | 40.5 ± 8.2  | 52.1 ± 8.2   |
| 16804635                 | <i>rplM</i> | 50S ribosomal protein L13    | 49.0 ± 4.6   | 60.7 ± 16.4   | 30.2 ± 2.2  | 61.7 ± 0.3   | 62.2 ± 4.1   | 83.4 ± 2.5    | 58.6 ± 2.5   | 24.8 ± 0.0   | 67.4 ± 5.0  | 81.6 ± 5.0   |
| 16804651                 | <i>rplO</i> | 50S ribosomal protein L15    | 24.6 ± 1.6   | 34.4 ± 22.5   | 53.8 ± 1.2  | 37.7 ± 2.4   | 30.3 ± 1.6   | 36.4 ± 0.0    | 52.8 ± 2.6   | 38.2 ± 7.7   | 38.2 ± 2.6  | 34.6 ± 2.6   |
| 16804663                 | <i>rplP</i> | 50S ribosomal protein L16    | 9.4 ± 1.4    | 20.3 ± 5.5    | 26.4 ± 2.3  | 6.5 ± 0.1    | 8.2 ± 2.9    | 12.5 ± 2.5    | 12.5 ± 2.5   | 25.0 ± 5.1   | 12.5 ± 2.5  | 10.7 ± 0.0   |
| 16804643                 | <i>rplQ</i> | 50S ribosomal protein L17    | 11.1 ± 3.1   | 20.6 ± 20.1   | 38.7 ± 5.2  | 10.4 ± 1.8   | 19.6 ± 3.1   | 20.8 ± 2.7    | 22.7 ± 5.4   | 28.4 ± 2.7   | 24.6 ± 2.7  | 17.0 ± 2.7   |

|                           |              |   |             |               |              |             |             |              |              |              |             |              |
|---------------------------|--------------|---|-------------|---------------|--------------|-------------|-------------|--------------|--------------|--------------|-------------|--------------|
| 16804654                  | <i>rplR</i>  | 50S ribosomal protein L18                         | 23.2 ± 0.1  | 32.4          | 37.5 ± 4.3   | 33.5 ± 1.2  | 34.1 ± 1.7  | 26.3 ± 6.2   | 41.7 ± 9.3   | 19.8 ± 9.3   | 13.2 ± 0.0  | 24.1 ± 3.1   |
| 16803827                  | <i>rplS</i>  | 50S ribosomal protein L19                         | 0.0         | 24.7 ± 17.7   | 12.4 ± 10.3  | 6.7 ± 2.0   | 6.3 ± 1.8   |              |              | 17.6 ± 6.2   | 4.4         | 4.4          |
| 16803582                  | <i>rplU</i>  | 50S ribosomal protein L21                         | 138.7 ± 8.0 | 345.4 ± 127.1 | 239.2 ± 11.3 | 222.3 ± 4.5 | 218.4 ± 4.8 | 174.6 ± 14.5 | 243.9 ± 32.7 | 151.5 ± 18.2 | 213.1 ± 3.6 | 195.1 ± 36.3 |
| 16804665                  | <i>rplV</i>  | 50S ribosomal protein L22                         | 27.5 ± 9.4  | 60.1 ± 32.7   | 38.1 ± 4.4   | 39.4 ± 2.7  | 34.6 ± 5.3  | 22.3 ± 0.0   | 26.7 ± 0.0   | 51.3 ± 3.2   | 24.5 ± 3.2  | 15.6 ± 3.2   |
| 16804668                  | <i>rplW</i>  | 50S ribosomal protein L23                         | 43.4 ± 4.2  | 106.4 ± 26.7  | 66.0 ± 1.4   | 56.4 ± 12.5 | 66.7 ± 0.2  | 52.8 ± 14.9  | 68.6 ± 7.5   | 58.0 ± 7.5   | 50.1 ± 3.7  | 39.6 ± 3.7   |
| 16804659                  | <i>rplX</i>  | 50S ribosomal protein L24                         | 25.7 ± 6.5  | 35.6 ± 23.6   | 31.9 ± 20.0  | 31.3 ± 3.8  | 38.4 ± 8.2  | 20.5 ± 0.0   | 25.7 ± 7.3   | 10.3         |             | 20.5         |
| 16802257                  | <i>ctc</i>   | 50S ribosomal protein L25                         | 14.9 ± 0.1  | 12.1 ± 7.2    | 14.4 ± 7.9   | 17.1 ± 0.3  | 21.2 ± 1.1  | 24.2 ± 1.8   | 25.4 ± 0.0   | 7.6          | 31.8 ± 1.8  | 34.3 ± 1.8   |
| 16803580                  | <i>rpmA</i>  | 50S ribosomal protein L27                         | 69.1 ± 11.1 | 96.1 ± 21.7   | 81.0 ± 1.8   | 85.1 ± 10.1 | 80.3 ± 2.5  | 82.1 ± 0.0   | 49.3 ± 7.7   | 43.8 ± 7.7   | 43.8 ± 15.5 | 43.8         |
| 16804662                  | <i>rpmC</i>  | 50S ribosomal protein L29                         | 89.0 ± 2.9  | 111.9 ± 46.8  | 79.7 ± 14.2  | 82.9 ± 8.4  | 62.5 ± 0.2  | 101.0 ± 0.0  | 73.8 ± 16.5  | 108.8 ± 11.0 | 73.8 ± 5.5  | 97.1 ± 5.5   |
| 16804586                  | <i>rpmE2</i> | 50S ribosomal protein L31                         | 67.2 ± 2.3  | 48.6 ± 20.3   | 52.7 ± 3.8   | 94.3 ± 1.9  | 81.7 ± 4.8  | 80.4 ± 0.0   | 74.2 ± 0.0   | 6.2 ± 0.0    | 71.1 ± 4.4  | 80.4 ± 8.7   |
| <b>t-RNA synthetase</b>   |              |   |             |               |              |             |             |              |              |              |             |              |
| 16802223                  | <i>metS</i>  | methionyl-tRNA synthetase                         | 0.9         | 4.2           | 11.7 ± 1.6   | 0.5         | 0.0         | 3.0 ± 1.1    | 2.7 ± 0.5    | 6.1 ± 0.0    | 10.6 ± 3.2  | 8.7 ± 0.5    |
| 16802274                  | <i>lysS</i>  | lysyl-tRNA synthetase                             | 3.8 ± 1.3   | 7.9 ± 3.3     | 11.4 ± 0.2   | 3.4 ± 1.4   | 3.2 ± 2.0   | 8.5 ± 3.5    | 8.5 ± 0.7    | 5.5 ± 2.1    | 16.5 ± 0.7  | 17.0 ± 4.3   |
| 16802283                  | <i>gltx</i>  | glutamyl-tRNA synthetase                          | 0.6         | 4.0 ± 1.7     | 7.0 ± 1.8    | 1.6 ± 0.5   | 0.3         | 2.1          | 2.1          | 2.6 ± 0.7    | 2.1 ± 0.0   | 3.1          |
| 16803262                  | <i>pheT</i>  | phenylalanyl-tRNA synthetase subunit beta         | 0.0         | 1.8           | 3.0          | 0.0         | 0.0         |              | 1.3          | 1.6 ± 0.5    | 0.7         |              |
| 16803498                  | <i>glyS</i>  | glycyl-tRNA synthetase subunit beta               | 0.0         | 2.7           | 1.7 ± 0.0    | 0.0         | 0.0         |              |              | 2.2          |             |              |
| 16803544                  | <i>alaS</i>  | alanyl-tRNA synthetase                            | 0.0         | 5.7 ± 0.4     | 8.4 ± 1.6    | 0.4         | 0.0         |              | 2.6 ± 1.2    | 7.0 ± 0.8    | 5.0 ± 0.4   | 5.6 ± 0.4    |
| 16803559                  | <i>aspS</i>  | aspartyl-tRNA synthetase                          | 1.0 ± 0.7   | 4.9 ± 1.3     | 6.4 ± 0.6    | 0.0         | 0.0         | 1.7          | 2.2 ± 0.6    | 3.9 ± 0.6    | 4.3         | 1.7 ± 0.0    |
| 16803647                  | <i>pheT</i>  | phenylalanyl-tRNA synthetase subunit beta         | 3.0         | 14.6 ± 3.9    | 7.3 ± 1.9    | 6.2 ± 2.1   | 5.2 ± 1.0   |              | 7.7 ± 3.6    | 11.6 ± 1.8   | 7.7 ± 0.0   | 5.1 ± 0.0    |
| 16803794                  | <i>gatB</i>  | aspartyl/glutamyl-tRNA amidotransferase subunit B | 3.5 ± 1.3   | 23.6 ± 8.1    | 28.9 ± 1.5   | 5.6 ± 0.6   | 5.9 ± 2.2   | 4.3 ± 3.1    | 10.8 ± 0.0   | 25.4 ± 3.8   | 16.8 ± 3.8  | 16.8 ± 5.4   |
| 16803795                  | <i>gatA</i>  | aspartyl/glutamyl-tRNA amidotransferase subunit A | 2.9 ± 0.5   | 4.8 ± 1.1     | 12.5 ± 0.3   | 3.3 ± 0.9   | 1.3         | 7.1 ± 0.8    | 7.1 ± 2.3    | 4.9 ± 0.8    | 13.7 ± 2.3  | 10.4 ± 0.8   |
| 16804058                  | <i>ileS</i>  | isoleucyl-tRNA synthetase                         | 0.3         | 2.0 ± 0.1     | 2.8 ± 0.5    | 0.0         | 0.2         | 1.4 ± 0.4    | 1.1 ± 0.0    | 1.7 ± 0.8    | 2.5 ± 0.4   | 3.6 ± 0.4    |
| 16804599                  | <i>argS</i>  | arginyl-tRNA synthetase                           | 1.1         | 3.4           | 4.2 ± 1.6    | 0.0         | 0.0         |              | 6.4          | 0.9          | 3.7 ± 0.0   | 6.9 ± 3.2    |
| <b>DNA/RNA polymerase</b> |              |   |             |               |              |             |             |              |              |              |             |              |
| 16802050                  | <i>dnaN</i>  | DNA polymerase III subunit beta                   | 1.6 ± 0.0   | 1.3           | 3.8 ± 1.0    | 1.7         | 1.2 ± 0.6   | 3.4 ± 1.0    | 4.7 ± 1.0    | 3.4 ± 1.0    | 4.7 ± 1.0   | 4.7 ± 1.0    |
| 16804644                  | <i>rpoA</i>  | DNA-directed RNA polymerase subunit alpha         | 2.9 ± 1.4   | 7.4 ± 2.5     | 10.3 ± 1.5   | 4.0 ± 0.1   | 4.3 ± 0.7   | 4.1 ± 3.5    | 8.2 ± 2.3    | 7.4 ± 1.2    | 8.2 ± 2.3   | 12.4 ± 1.2   |
| 16802304                  | <i>rpoB</i>  | DNA-directed RNA polymerase subunit beta          | 3.2 ± 0.9   | 7.7 ± 0.5     | 11.4 ± 0.2   | 0.8 ± 0.4   | 0.6 ± 0.2   | 8.9 ± 0.3    | 6.9 ± 0.6    | 6.5 ± 0.6    | 5.2 ± 2.5   | 7.8 ± 0.0    |
| 16802305                  | <i>rpoC</i>  | DNA-directed RNA polymerase subunit beta'         | 5.0 ± 1.0   | 17.8 ± 3.5    | 20.4 ± 0.9   | 1.7 ± 0.6   | 1.0 ± 0.3   | 10.9 ± 1.5   | 13.7 ± 1.2   | 11.5 ± 1.8   | 10.5 ± 0.3  | 11.7 ± 0.9   |

|                  |             |   |            |               |              |             |             |              |             |              |              |             |
|------------------|-------------|---|------------|---------------|--------------|-------------|-------------|--------------|-------------|--------------|--------------|-------------|
| 16804598         | <i>rpoZ</i> | DNA-directed RNA polymerase subunit delta | 4.1 ± 1.1  | 6.2 ± 2.1     | 11.2 ± 7.0   | 5.9 ± 1.1   | 4.0 ± 1.1   | 8.4 ± 0.0    | 12.6 ± 2.0  | 2.8          | 8.4 ± 3.9    | 11.2 ± 0.0  |
| 16803866         | <i>rpoE</i> | DNA-directed RNA polymerase subunit omega | 4.4 ± 0.0  | 0.0           | 0.0          | 4.7         | 8.7         |              |             |              |              |             |
| <b>Helicase</b>  |             |   |            |               |              |             |             |              |             |              |              |             |
| 16803799         | <i>pcrA</i> | ATP-dependent DNA helicase                | 0.0        | 0.0           | 0.0          | 0.0         | 0.0         |              |             |              | 1.4          | 1.4         |
| 16802907         |             | ATP-dependent RNA helicase                | 15.9 ± 1.7 | 39.6 ± 8.9    | 31.9 ± 0.9   | 2.7 ± 1.2   | 2.6 ± 2.0   | 41.6 ± 2.1   | 36.1 ± 4.3  | 23.6 ± 0.7   | 22.1 ± 0.0   | 16.6 ± 2.1  |
| 16803490         |             | DEAD/DEAH box helicase                    | 2.4 ± 1.4  | 1.1           | 0.0          | 0.0         | 0.0         | 7.0 ± 3.3    | 2.3 ± 0.0   |              | 1.2          |             |
| <b>Cofactors</b> |             |   |            |               |              |             |             |              |             |              |              |             |
| 16803362         | <i>nusA</i> | transcription elongation factor NusA      | 8.1 ± 0.0  | 18.5 ± 6.3    | 19.6 ± 1.5   | 6.7 ± 1.1   | 4.4 ± 1.7   | 15.9 ± 2.9   | 16.5 ± 0.0  | 15.9 ± 1.0   | 13.8 ± 0.0   | 13.1 ± 2.9  |
| 16803536         | <i>greA</i> | transcription elongation factor GreA      | 16.4 ± 1.3 | 11.4 ± 7.5    | 7.6          | 25.1 ± 1.9  | 9.4 ± 5.3   | 16.4 ± 0.0   | 16.4 ± 0.0  |              | 23.0         | 27.9 ± 7.0  |
| 16804648         | <i>infA</i> | translation initiation factor IF-1        | 18.5 ± 2.8 | 15.1 ± 12.2   | 31.9 ± 0.7   | 29.9 ± 5.5  | 32.2 ± 0.1  | 24.5 ± 5.0   | 24.5 ± 5.0  | 7.0          | 24.5 ± 5.0   | 21.0 ± 9.9  |
| 16803365         | <i>infB</i> | translation initiation factor IF-2        | 1.2 ± 0.6  | 3.0 ± 0.7     | 4.3 ± 0.6    | 0.4 ± 0.0   | 0.2         | 3.4 ± 1.0    | 5.1 ± 0.5   | 2.7 ± 1.0    | 5.1 ± 0.5    | 5.4 ± 1.9   |
| 16803825         | <i>infC</i> | translation initiation factor IF-3        | 10.3 ± 0.0 | 20.3 ± 13.5   | 13.3 ± 0.3   | 12.6 ± 2.8  | 11.8 ± 0.0  | 7.3 ± 2.1    | 11.7 ± 8.3  | 8.8 ± 0.0    | 13.2 ± 2.1   | 14.7 ± 4.1  |
| 16803697         | <i>tsf</i>  | elongation factor Ts                      | 34.2 ± 1.6 | 63.8 ± 2.8    | 74.2 ± 1.6   | 70.0 ± 4.4  | 71.0 ± 1.2  | 52.9 ± 5.0   | 75.8 ± 2.5  | 57.3 ± 1.2   | 83.8 ± 11.2  | 100.5 ± 5.0 |
| 16804690         | <i>tuf</i>  | elongation factor Tu                      | 75.7 ± 3.6 | 295.1 ± 181.6 | 539.3 ± 18.1 | 115.5 ± 6.3 | 124.4 ± 4.7 | 164.7 ± 15.0 | 282.9 ± 1.9 | 523.2 ± 22.5 | 411.0 ± 40.4 | 333.3 ± 7.5 |
| 16804691         | <i>fus</i>  | elongation factor G                       | 14.1 ± 1.3 | 64.3 ± 15.5   | 80.8 ± 5.5   | 9.6 ± 2.8   | 6.9 ± 1.2   | 25.5 ± 3.2   | 36.7 ± 1.1  | 55.4 ± 4.2   | 41.6 ± 4.8   | 41.9 ± 4.2  |
| 16803107         |             | GTP-binding elongation factor             | 5.9 ± 0.7  | 9.2 ± 1.0     | 9.5 ± 1.6    | 0.5         | 0.2         | 10.9 ± 0.0   | 9.2 ± 1.2   | 8.4 ± 2.4    | 5.0 ± 0.0    | 3.3 ± 0.0   |
| 16804581         | <i>prfA</i> | peptide chain release factor 1            | 0.8        | 0.0           | 0.0          | 4.3 ± 0.1   | 2.4 ± 0.0   |              |             | 1.4          | 4.2 ± 2.0    | 2.8 ± 2.0   |
| 16803091         | <i>def</i>  | peptide deformylase                       | 0.0        | 0.0           | 3.2          | 10.3 ± 5.0  | 6.4 ± 4.5   |              |             |              | 5.6 ± 0.0    | 8.4         |
| 16802259         | <i>pth</i>  | peptidyl-tRNA hydrolase                   | 0.0        | 0.0           | 0.0          | 1.7 ± 0.0   | 1.6         |              |             |              | 2.7          |             |
| <b>Etc</b>       |             |   |            |               |              |             |             |              |             |              |              |             |
| 16803354         | <i>frr</i>  | ribosome recycling factor                 | 35.9 ± 0.1 | 6.2 ± 2.1     | 6.2          | 42.4 ± 3.2  | 31.1 ± 3.3  | 34.7 ± 2.0   | 44.4 ± 3.9  |              | 44.4 ± 0.0   | 54.2 ± 2.0  |
| 16803511         | <i>prmA</i> | ribosomal protein L11 methyltransferase   | 0.0        | 0.0           | 1.9          | 0.0         | 0.0         | 3.3 ± 0.0    | 1.7         |              | 1.7          |             |

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**Supplementary Table 7.** The summary of the transport-related proteins expressions

| GI              | Gene | Product   | Exponential |             |            |            |            | Stationary |             |             |            |            |
|-----------------|------|---|-------------|-------------|------------|------------|------------|------------|-------------|-------------|------------|------------|
|                 |      |   | 10°C        | 20°C        | 30°C       | 37°C       | 42°C       | 10°C       | 20°C        | 30°C        | 37°C       | 42°C       |
| <b>PTS type</b> |      |   |             |             |            |            |            |            |             |             |            |            |
| 16802144        |      | PTS mannose transporter subunit IIAB                | 12.1 ± 0.7  | 23.8 ± 5.8  | 19.6 ± 3.5 | 16.5 ± 1.0 | 12.3 ± 0.0 | 20.5 ± 1.2 | 28.8 ± 1.2  | 11.5 ± 4.6  | 15.6 ± 1.2 | 23.8 ± 5.8 |
| 16802146        |      | PTS mannose transporter subunit IID                 | 12.6 ± 0.8  | 40.7 ± 12.7 | 30.3 ± 0.7 | 4.2 ± 0.1  | 4.9 ± 0.0  | 23.2 ± 1.2 | 27.5 ± 2.4  | 26.7 ± 1.2  | 24.1 ± 0.0 | 24.1 ± 2.4 |
| 16803057        |      | PTS glucose transporter subunit IIA                 | 4.8 ± 1.3   | 0.0         | 0.0        | 6.9 ± 1.3  | 4.7 ± 1.3  |            | 6.5         |             | 8.1 ± 2.3  | 6.5 ± 4.6  |
| 16803135        |      | PTS cellbiose transporter subunit IIB               | 0.0         | 0.0         | 0.0        | 2.4        | 2.3        |            |             |             |            |            |
| 16804411        |      | PTS beta-glucoside transporter subunit IIB          | 42.2 ± 8.4  | 36.0 ± 10.7 | 37.9 ± 3.3 | 28.2 ± 5.0 | 28.0 ± 2.0 | 48.8 ± 3.6 | 43.6 ± 10.9 | 41.1 ± 0.0  | 41.1 ± 7.3 | 38.5 ± 3.6 |
| 16804720        |      | PTS cellbiose transporter subunit IIB               | 10.9 ± 2.2  | 0.0         | 0.0        | 3.3        | 0.0        | 23.7 ± 3.7 |             |             |            |            |
| 16803043        |      | phosphotransferase system enzyme I                  | 12.8 ± 0.8  | 25.8 ± 1.5  | 33.1 ± 2.2 | 7.0 ± 2.1  | 5.2 ± 0.0  | 28.7 ± 1.9 | 28.7 ± 3.2  | 16.4 ± 1.3  | 28.7 ± 4.5 | 29.6 ± 3.2 |
| <b>ABC type</b> |      |   |             |             |            |            |            |            |             |             |            |            |
| 16802183        |      | peptide ABC transporter substrate-binding protein   | 2.0 ± 0.4   | 12.9 ± 5.4  | 17.9 ± 2.8 | 2.1 ± 0.5  | 2.0 ± 1.2  | 3.9        | 8.4 ± 4.9   | 9.9 ± 0.0   | 2.5 ± 0.7  | 4.4 ± 2.1  |
| 16803054        |      | glycine/betaine ABC transporter ATP-binding protein | 1.9 ± 0.6   | 8.5         | 8.2 ± 0.9  | 1.6 ± 1.1  | 1.5 ± 0.0  | 7.3 ± 0.9  | 7.3 ± 2.8   | 4.0 ± 0.0   | 4.0        | 4.6 ± 2.8  |
| 16804153        |      | ABC transporter ATP-binding protein                 | 3.6 ± 1.7   | 15.0        | 12.7 ± 1.4 | 8.0 ± 0.7  | 4.7 ± 1.6  | 11.2 ± 4.3 | 18.3 ± 0.0  | 5.1 ± 4.3   | 25.4 ± 7.2 | 23.4 ± 1.4 |
| 16804232        |      | peptide ABC transporter ATP-binding protein         | 1.7         | 6.7         | 6.6 ± 2.5  | 1.8 ± 0.0  | 1.2 ± 0.6  | 2.9        | 3.6 ± 1.0   | 7.2 ± 2.0   | 2.9        | 2.2 ± 1.0  |
| 16804453        |      | ABC transporter ATP-binding protein                 | 5.8 ± 1.7   | 17.6 ± 6.0  | 22.4 ± 5.9 | 9.0 ± 0.7  | 6.8 ± 0.0  | 9.9 ± 0.0  | 20.7 ± 1.4  | 25.7 ± 11.2 | 24.7 ± 4.2 | 22.7 ± 7.0 |
| <b>Etc</b>      |      |   |             |             |            |            |            |            |             |             |            |            |
| 16804398        |      | transmembrane protein                               | 2.4 ± 0.0   | 2.6 ± 0.6   | 5.0 ± 0.4  | 0.5 ± 0.3  | 0.9 ± 0.2  |            | 1.5 ± 0.4   | 1.2 ± 0.0   |            |            |

**Supplementary Table 8.** The summary of protease expressions

| GI       | Gene | Product   | Exponential |           |          |          |          | Stationary |          |          |          |          |
|----------|------|---|-------------|-----------|----------|----------|----------|------------|----------|----------|----------|----------|
|          |      |   | 10°C        | 20°C      | 30°C     | 37°C     | 42°C     | 10°C       | 20°C     | 30°C     | 37°C     | 42°C     |
| 16803651 |      | aminopeptidase                                  | 2.2±0.6     | 4.1       | 5.1±0.1  | 3.6±0.1  | 3.0±1.8  | 4.4±0.0    | 7.4±2.1  | 4.4±2.1  | 4.4±0.0  | 5.2±1.0  |
| 16803751 |      | aminopeptidase                                  | 6.0±0.0     | 14.7±0.7  | 15.3±0.7 | 1.9±0.5  | 1.8±0.5  | 11.5±0.0   | 11.5±3.6 | 10.9±0.9 | 10.2±3.6 | 8.3±0.9  |
| 16803394 |      | aminopeptidase P                                | 0.0         | 3.9±1.6   | 5.9±1.3  | 0.0      | 0.0      | 2.2±1.0    | 6.6±3.1  | 3.7±3.1  |          |          |
| 16803820 |      | aminotripeptidase                               | 1.5±0.0     | 4.4±2.9   | 2.1±1.0  | 0.8      | 1.1±0.5  | 3.8        | 3.8±1.8  | 1.3      | 3.8±0.0  | 3.8±1.8  |
| 16804245 | clpB | Clp protease subunit B                          | 0.0         | 1.5±0.6   | 3.7±0.4  | 4.9±0.2  | 6.1±0.5  |            |          | 4.4±1.3  | 20.3±0.4 | 26.0±1.7 |
| 16802278 | clpC | endopeptidase Clp ATP-binding chain C           | 0.0         | 2.3       | 2.2±0.0  | 0.4±0.0  | 0.0      | 1.9±0.9    | 0.9±0.4  | 4.4±0.9  | 7.3±1.3  | 6.6±1.3  |
| 16803178 | clpP | ATP-dependent Clp protease proteolytic subunit  | 1.6±0.0     | 3.5±1.5   | 6.0      | 14.0±3.8 | 12.4±0.0 | 2.7±0.0    | 2.7±0.0  | 6.7±1.9  | 25.6±1.9 | 27.0±0.0 |
| 16804506 | clpP | ATP-dependent Clp protease proteolytic subunit  | 3.1         | 4.9       | 16.6±6.1 | 8.9±1.0  | 10.7±2.2 | 9.3±1.9    | 8.0±3.8  | 5.3      | 16.0±3.8 | 12.0±1.9 |
| 16803308 | clpX | ATP-dependent protease ATP-binding subunit ClpX | 0.7         | 12.6      | 10.6±1.2 | 0.8±0.0  | 0.0      | 3.1±0.9    | 6.2±0.0  | 6.8±0.9  | 8.1±4.4  | 8.1±4.4  |
| 16803660 | pepV | dipeptidase PepV                                | 3.6±0.5     | 16.3±11.5 | 11.3±5.1 | 1.0±0.5  | 2.9±0.5  | 7.8±0.0    | 9.4±2.4  | 8.3±2.4  | 7.2±0.8  | 5.6±0.0  |
| 16802625 |      | invasion associated secreted endopeptidase      | 0.7         | 0.0       | 0.0      | 0.0      | 0.3      |            |          |          | 1.1      | 3.4±1.6  |
| 16803749 |      | methionine aminopeptidase                       | 1.8±0.9     | 14.4±4.3  | 11.7±0.3 | 6.3±0.1  | 5.9±1.7  | 3.1±1.5    | 7.2±1.5  | 12.4±0.0 | 10.3±0.0 | 12.4±2.9 |
| 16803001 |      | protease  | 0.0         | 0.0       | 0.0      | 0.0      | 0.0      |            |          |          | 1.3      | 1.3      |
| 16803618 |      | X-Pro dipeptidase                               | 1.7         | 2.6       | 5.7±1.0  | 0.9±0.0  | 1.2±0.6  | 4.3±2.0    | 7.1      | 5.0±3.0  | 2.9±0.0  | 4.3      |
| 16803257 |      | Glytamyl aminopeptidase                         | 0.0         | 0.0       | 2.5±1.1  | 0.0      | 0.0      | 3.0±0.0    | 2.2±1.0  | 1.5±0.0  |          | 1.5      |

**Supplementary Table 9.** The summary of functional protein expressions

| GI                           | Gene  | Product   | Exponential  |               |              |              |              | Stationary   |             |              |             |              |
|------------------------------|-------|---|--------------|---------------|--------------|--------------|--------------|--------------|-------------|--------------|-------------|--------------|
|                              |       |   | 10°C         | 20°C          | 30°C         | 37°C         | 42°C         | 10°C         | 20°C        | 30°C         | 37°C        | 42°C         |
| <b>Motility</b>              |       |   |              |               |              |              |              |              |             |              |             |              |
| 16803739                     | cheV  | chemotaxis protein                                      | 11.3 ± 1.4   | 4.8           | 0.0          | 0.0          | 0.0          | 20.0 ± 3.7   | 6.1 ± 1.2   |              |             |              |
| 16804059                     | cheY  | chemotaxis protein CheY                                 | 12.5 ± 3.6   | 17.4 ± 2.5    | 16.1 ± 4.2   | 19.9 ± 0.8   | 14.7 ± 2.3   | 17.0 ± 4.0   | 11.3 ± 4.0  | 12.7 ± 2.0   | 24.1 ± 2.0  | 25.5 ± 4.0   |
| 16802732                     | flaA  | flagellin   | 300.6 ± 0.4  | 88.5 ± 1.9    | 46.3 ± 5.6   | 0.0          | 0.0          | 323.5 ± 2.7  | 81.3 ± 2.7  | 27.4 ± 6.7   |             |              |
| 16802739                     | flgE  | flagellar hook protein FlgE                             | 9.1 ± 0.6    | 5.3 ± 2.2     | 0.0          | 0.0          | 0.0          | 14.8 ± 0.0   | 8.7 ± 1.0   |              |             |              |
| 16804330                     |       | major tail shaft protein                                | 18.3 ± 1.6   | 7.9 ± 6.4     | 8.3 ± 0.2    | 0.0          | 0.0          | 23.8 ± 2.6   | 20.1 ± 2.6  | 12.8 ± 7.8   |             |              |
| <b>REDOX</b>                 |       |   |              |               |              |              |              |              |             |              |             |              |
| 16804516                     | trxB  | thioredoxin reductase                                   | 0.0          | 4.6           | 3.8 ± 0.1    | 0.0          | 2.9          |              | 5.0         | 3.4          | 6.7 ± 2.4   | 10.1 ± 2.4   |
| 16804191                     | trxA  | thioredoxin   | 13.6 ± 3.8   | 18.2 ± 7.6    | 10.7         | 14.1 ± 3.7   | 8.0 ± 3.8    | 4.6 ± 0.0    | 18.5        |              | 11.6 ± 3.3  | 9.3          |
| 16803273                     | trxA  | thioredoxin   | 17.5 ± 0.1   | 17.5 ± 1.0    | 39.5 ± 0.9   | 21.2 ± 0.4   | 21.4 ± 2.0   | 37.2 ± 3.5   | 37.2 ± 3.5  | 29.7 ± 0.0   | 44.6 ± 0.0  | 49.6 ± 7.0   |
| 16803644                     |       | 2-cys peroxiredoxin                                     | 1.7 ± 0.0    | 7.5 ± 3.1     | 6.5 ± 0.1    | 2.6 ± 1.2    | 2.5 ± 1.2    |              | 2.9 ± 0.0   | 4.3 ± 2.0    | 4.3 ± 2.0   | 7.2 ± 2.0    |
| 16804676                     |       | NADH dehydrogenase                                      | 6.2 ± 2.0    | 15.0 ± 7.5    | 23.7 ± 0.1   | 5.5 ± 0.8    | 4.9 ± 1.0    | 12.3 ± 0.0   | 16.3 ± 1.2  | 19.2 ± 0.6   | 14.7 ± 1.2  | 15.5 ± 1.2   |
| 16804427                     |       | NADH dehydrogenase                                      | 0.0          | 1.2           | 3.7 ± 1.1    | 0.0          | 1.5          | 2.6          | 1.3         | 5.9 ± 0.9    | 2.6 ± 0.0   | 4.6 ± 0.9    |
| 16804509                     |       | NADPH dehydrogenase                                     | 0.9 ± 0.0    | 2.0 ± 0.9     | 3.5 ± 0.1    | 1.9          | 1.3 ± 0.6    | 3.9 ± 1.1    | 2.3 ± 1.1   |              |             |              |
| 16802400                     |       | fumarate reductase subunit A                            | 3.7 ± 1.8    | 26.0 ± 6.4    | 57.0 ± 11.5  | 7.7 ± 1.1    | 8.8 ± 0.5    | 4.8 ± 0.7    | 10.6 ± 3.0  | 34.4 ± 2.2   | 11.1 ± 2.2  | 11.1 ± 2.2   |
| <b>Protein Translocation</b> |       |   |              |               |              |              |              |              |             |              |             |              |
| 16804548                     | secA  | preprotein translocase subunit SecA                     | 2.1 ± 0.5    | 2.1 ± 1.4     | 4.8 ± 2.8    | 0.0          | 0.0          | 4.0 ± 1.3    | 4.0 ± 0.4   | 3.6 ± 0.9    | 4.0 ± 1.3   | 2.7 ± 0.4    |
| 16803567                     | secDF | preprotein translocase SecDF                            | 0.0          | 0.6           | 1.6 ± 0.0    | 0.0          | 0.0          |              |             | 1.4          |             |              |
| 16804489                     | secG  | preprotein translocase subunit SecG                     | 0.0          | 9.3 ± 3.9     | 8.1 ± 0.2    | 0.0          | 0.0          |              |             |              | 7.1         |              |
| <b>Secondary Metabolite</b>  |       |   |              |               |              |              |              |              |             |              |             |              |
| 16804602                     |       | 4-oxalocrotonate isomerase                              | 14.7 ± 0.1   | 0.0           | 19.0 ± 0.4   | 12.7 ± 3.3   | 7.2          | 8.3          | 16.7        | 8.3 ± 0.0    |             |              |
| 16803640                     | aroA  | 3-deoxy-7-phosphoheptulonate synthase/chorismate mutase | 4.3 ± 1.2    | 4.6 ± 3.0     | 5.8 ± 1.3    | 1.8 ± 1.3    | 1.7 ± 0.0    | 6.5 ± 3.1    | 11.6 ± 2.0  | 5.1 ± 1.0    | 5.1 ± 1.0   | 6.5 ± 1.0    |
| 16804452                     | menB  | naphthoate synthase                                     | 2.8 ± 0.0    | 7.5 ± 4.9     | 8.1 ± 3.7    | 5.5 ± 0.6    | 4.8 ± 0.0    | 7.2 ± 1.7    | 11.4 ± 2.5  | 9.6 ± 0.0    | 6.0 ± 1.7   | 9.6 ± 3.4    |
| 16803713                     | menB  | naphthoate synthase                                     | 5.1 ± 0.8    | 12.5 ± 5.2    | 9.8 ± 1.3    | 1.7 ± 0.8    | 0.5          | 10.5 ± 1.4   | 7.7 ± 2.7   | 6.7 ± 1.4    | 4.8 ± 1.4   | 2.9 ± 1.4    |
| <b>Signaling / Regulator</b> |       |   |              |               |              |              |              |              |             |              |             |              |
| 16803639                     | ccpA  | catabolite control protein A                            | 3.6          | 28.7 ± 4.1    | 21.3 ± 8.0   | 4.8 ± 1.4    | 4.5 ± 0.0    | 11.7 ± 1.1   | 17.9 ± 3.3  | 15.5 ± 4.4   | 9.3 ± 2.2   | 6.2          |
| 16803042                     | ptsH  | ptsH:p, phosphocarrier protein HPr                      | 384.6 ± 32.0 | 564.6 ± 184.5 | 250.5 ± 5.4  | 568.8 ± 17.8 | 589.0 ± 24.1 | 238.6 ± 17.3 | 214.1 ± 8.7 | 165.2 ± 17.3 | 183.5 ± 8.7 | 211.0 ± 38.9 |
| 16802932                     | rsbT  | positive regulation of sigma-B activity                 | 12.6 ± 1.7   | 10.2 ± 4.3    | 6.6 ± 3.0    | 15.5 ± 4.8   | 12.4 ± 1.6   | 15.6 ± 5.5   | 3.9 ± 0.0   |              | 3.9         | 5.9 ± 2.8    |
| 16802243                     | spoVG | regulatory protein SpoVG                                | 146.7 ± 1.5  | 264.1 ± 110.4 | 172.4 ± 28.1 | 178.5 ± 7.9  | 152.2 ± 2.5  | 214.4 ± 32.1 | 216.9 ± 7.1 | 181.6 ± 0.0  | 216.9 ± 7.1 | 234.6 ± 17.8 |

|          |       |   |            |             |            |            |            |            |            |           |             |            |
|----------|-------|---|------------|-------------|------------|------------|------------|------------|------------|-----------|-------------|------------|
| 16802242 | spoVG | regulatory protein SpoVG                | 24.1 ± 0.1 | 36.0 ± 10.7 | 11.7 ± 0.3 | 34.4 ± 3.8 | 28.0 ± 2.0 | 23.1 ± 3.6 | 20.5 ± 0.0 | 10.3      | 33.4 ± 10.9 | 28.2 ± 3.6 |
| 16803320 | codY  | transcriptional repressor CodY          | 6.5 ± 0.9  | 0.0         | 9.1 ± 0.2  | 6.7 ± 0.7  | 5.2 ± 0.8  | 8.0 ± 0.0  | 12.0 ± 2.8 | 7.0 ± 1.4 | 11.0 ± 1.4  | 9.0 ± 1.4  |
| 16803841 | ffh   | signal recognition particle protein Ffh | 0.7        | 4.3         | 4.0 ± 1.9  | 1.4 ± 1.0  | 1.3        | 1.2        | 1.7 ± 0.8  | 1.2       | 5.2 ± 0.8   | 5.8 ± 1.6  |
| 16802935 | rsbW  | serine-protein kinase RsbW              | 7.7 ± 0.0  | 9.1         | 16.9 ± 8.3 | 6.1        | 4.7 ± 1.3  | 9.9 ± 4.6  | 11.5 ± 2.3 | 9.9 ± 0.0 | 6.6 ± 4.6   | 13.1       |
| 16803976 | engA  | GTP-binding protein EngA                | 2.8 ± 1.0  | 3.2         | 2.6 ± 1.8  | 0.0        | 0.0        | 4.1 ± 0.8  | 5.3 ± 2.5  | 1.8 ± 0.8 | 7.0 ± 1.7   | 3.5        |

### Nucleotide metabolism

|          |      |  |            |             |            |            |            |            |            |            |            |            |
|----------|------|--|------------|-------------|------------|------------|------------|------------|------------|------------|------------|------------|
| 16803564 | apt  | adenine phosphoribosyltransferase                  | 12.3 ± 2.5 | 18.4 ± 2.7  | 13.7 ± 5.1 | 3.7 ± 0.1  | 3.5        | 21.0 ± 0.0 | 19.5 ± 6.4 | 10.5 ± 6.4 | 6.0 ± 0.0  | 7.5 ± 2.1  |
| 16804649 | adk  | adenylate kinase                                   | 7.0 ± 0.0  | 0.0         | 18.9 ± 3.4 | 18.9 ± 2.4 | 14.3 ± 2.9 | 8.3 ± 1.7  | 13.1 ± 5.0 | 4.8        | 15.4 ± 1.7 | 16.6 ± 0.0 |
| 16804576 | upp, | uracil phosphoribosyltransferase                   | 16.2 ± 6.3 | 30.9 ± 4.4  | 34.2 ± 3.3 | 19.1 ± 2.9 | 18.0 ± 3.0 | 23.9 ± 1.8 | 25.1 ± 7.1 | 26.4 ± 1.8 | 21.3 ± 8.9 | 22.6 ± 0.0 |
| 16803896 | pnp  | purine nucleoside phosphorylase                    | 6.7 ± 1.9  | 16.3 ± 6.6  | 16.8 ± 2.2 | 4.1        | 2.6 ± 0.0  | 13.6 ± 0.0 | 18.2 ± 3.2 | 10.2 ± 1.6 | 4.5        |            |
| 16803992 | deoD | purine nucleoside phosphorylase                    | 3.4        | 10.2 ± 4.3  | 4.5        | 1.2 ± 0.0  | 1.1        | 2.9 ± 1.4  | 3.9        | 1.9        |            |            |
| 16802704 | thiD | phosphomethylpyrimidine kinase                     | 8.2        | 12.1 ± 6.8  | 10.2 ± 1.8 | 4.9 ± 1.8  | 4.6 ± 1.6  | 3.0 ± 1.4  | 9.0 ± 1.4  | 9.0 ± 4.2  | 7.0 ± 1.4  | 6.0 ± 2.8  |
| 16803371 | pnpA | polynucleotide phosphorylase                       | 3.2 ± 1.5  | 11.3 ± 4.7  | 7.0 ± 1.9  | 1.1 ± 0.3  | 1.0 ± 0.3  | 6.1 ± 0.5  | 6.1 ± 1.5  | 3.3 ± 0.5  | 4.7 ± 1.5  | 5.4 ± 0.5  |
| 16804795 | guaB | inosine-monophosphate dehydrogenase                | 4.2 ± 1.4  | 7.9 ± 5.9   | 18.7 ± 0.4 | 9.0 ± 0.3  | 11.0 ± 1.4 | 6.0 ± 0.8  | 11.5 ± 2.3 | 17.0 ± 0.8 | 20.3 ± 0.8 | 20.3 ± 2.3 |
| 16804526 | uvrA | excinuclease ABC subunit A                         | 0.0        | 1.0         | 2.8 ± 1.2  | 1.0        | 0.0        | 0.5        |            | 1.1 ± 0.8  | 3.5 ± 1.1  | 8.1 ± 0.8  |
| 16804527 | uvrB | excinuclease ABC subunit B                         | 0.0        | 0.0         | 0.0        | 0.0        | 0.0        |            |            |            | 3.0 ± 1.1  |            |
| 16804194 |      | ribonucleotide-diphosphate reductase subunit alpha | 0.8 ± 0.6  | 2.9 ± 1.0   | 9.4 ± 0.3  | 0.8 ± 0.0  | 0.2        | 3.3 ± 0.9  | 3.3 ± 0.9  | 7.2 ± 0.9  | 5.3 ± 0.0  | 4.0 ± 0.9  |
| 16804193 | nrdF | ribonucleotide-diphosphate reductase subunit beta  | 2.5        | 1.3         | 22.0 ± 1.6 | 3.5 ± 1.3  | 0.0        | 3.6 ± 1.0  | 5.7 ± 0.0  | 9.3 ± 1.0  | 19.3 ± 3.0 | 29.3 ± 7.1 |
| 16802245 | prs  | ribose-phosphate pyrophosphokinase                 | 7.2 ± 0.7  | 22.9 ± 11.0 | 23.4 ± 4.5 | 1.0        | 2.8 ± 1.3  | 13.1 ± 0.0 | 15.6 ± 3.5 | 15.6 ± 3.5 | 13.1 ± 2.3 | 15.6 ± 1.2 |
| 16802325 |      | anaerobic ribonucleoside triphosphate reductase    | 3.9 ± 0.9  | 4.0 ± 1.1   | 9.6 ± 2.1  | 0.0        | 0.0        | 6.4 ± 0.0  | 5.7 ± 1.0  | 4.6 ± 1.5  | 2.1 ± 0.0  | 2.5 ± 0.5  |

### Cell Wall structure

|          |      |  |            |             |            |            |            |            |            |            |            |            |
|----------|------|--|------------|-------------|------------|------------|------------|------------|------------|------------|------------|------------|
| 16803012 | dltC | D-alanine--poly(phosphoribitol) ligase subunit 2 | 24.4 ± 2.6 | 29.4        | 29.1 ± 0.6 | 31.2 ± 6.1 | 29.4 ± 0.1 | 12.8 ± 0.0 | 31.9 ± 0.0 | 12.8 ± 0.0 | 19.2 ± 9.0 | 35.1 ± 4.5 |
| 16804543 | spl  | peptidoglycan lytic protein P45                  | 0.0        | 0.0         | 0.0        | 0.8        | 4.3 ± 0.6  |            |            | 6.1 ± 1.0  | 10.1 ± 1.0 | 11.4 ± 2.9 |
| 16804414 |      | peptidyl-prolyl cis-trans isomerase              | 15.8 ± 2.3 | 36.4 ± 13.0 | 19.9 ± 2.6 | 14.8 ± 0.3 | 14.7 ± 1.0 | 24.2 ± 3.8 | 24.2 ± 0.0 | 17.5 ± 5.7 | 22.8 ± 1.9 | 16.1 ± 3.8 |
| 16802177 | ncsE | N-acetylmuramoyl-L-alanine amidase               | 2.5 ± 1.8  | 8.5 ± 3.6   | 9.9 ± 0.2  | 0.0        | 0.6        |            |            | 4.3 ± 0.0  |            |            |

### DNA/RNA

|          |     |                               |              |               |             |               |               |               |              |             |              |             |
|----------|-----|-------------------------------|--------------|---------------|-------------|---------------|---------------|---------------|--------------|-------------|--------------|-------------|
| 16802093 | ssb | single-strand binding protein | 4.3 ± 1.2    | 0.0           | 6.6         | 0.0           | 0.0           | 5.9 ± 4.2     | 2.9          |             |              |             |
| 16803973 | hup | DNA-binding protein HU        | 1399.0 ± 4.2 | 392.4 ± 346.0 | 686.9 ± 3.8 | 2259.0 ± 57.1 | 2266.9 ± 49.9 | 1446.3 ± 65.7 | 839.3 ± 37.0 | 551.8 ± 8.2 | 897.4 ± 53.4 | 917.7 ± 0.0 |

### 기타

|          |  |                                |            |           |           |           |     |            |           |           |     |           |
|----------|--|--------------------------------|------------|-----------|-----------|-----------|-----|------------|-----------|-----------|-----|-----------|
| 16803619 |  | alanine dehydrogenase          | 1.3 ± 0.6  | 3.8 ± 1.6 | 5.0 ± 0.1 | 3.1 ± 0.7 | 0.4 | 7.3 ± 2.1  | 9.4 ± 5.1 | 6.5 ± 1.0 | 1.5 | 3.6 ± 1.0 |
| 16803220 |  | carboxysome structural protein | 30.9 ± 2.4 | 10.5      | 7.0 ± 0.2 | 0.0       | 0.0 | 21.6 ± 4.4 |           |           |     |           |



