Assessment of CcpA-mediated catabolite control of gene expression in Bacillus cereus ATCC 14579

van der Voort, Menno; Kuipers, Oscar P.; Buist, Girbe; de Vos, Willem M.; Abee, Tjakko

Published in:
BMC Microbiology

DOI:
10.1186/1471-2180-8-62

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version
Publisher's PDF, also known as Version of record

Publication date:
2008

Link to publication in University of Groningen/UMCG research database

Citation for published version (APA):
vanderVoort, M., Kuipers, O. P., Buist, G., de Vos, W. M., & Abee, T. (2008). Assessment of CcpA-mediated catabolite control of gene expression in Bacillus cereus ATCC 14579. BMC Microbiology, 8(1), Article 62. https://doi.org/10.1186/1471-2180-8-62

Copyright
Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

The publication may also be distributed here under the terms of Article 25fa of the Dutch Copyright Act, indicated by the "Taverne" license. More information can be found on the University of Groningen website: https://www.rug.nl/library/open-access/self-archiving-pure/taverne-amendment.

Take-down policy
If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): http://www.rug.nl/research/portal. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.
Table S1: Differentially expressed genes in the ccpA deletion strain as compared to the wild type in early- and mid-exponential phase.

| RZC nr. | BC nr. | Array ratio early-exp* | Array ratio mid-exp* | qPCR ratio early-exp† | Alias | Annotation | CRE-site‡ |
|---------|--------|------------------------|----------------------|----------------------|-------|------------|-----------|
| RZC01285 | BC0197 | 4.10                   | 2.91                 |                      |       | ABC transporter ATP-binding protein | -        |
| RZC04643 | BC0311 | 1.43                   | 2.51                 |                      |       | hypothetical protein               | -        |
| RZC02596 | BC0372 | 3.43                   | 2.62                 |                      |       | hypothetical protein               | +        |
| RZC03161 | BC0378 | 6.58                   | 9.43                 |                      | fclK  | 5-methylthioribose kinase           | 1        |
| RZC02455 | BC0379 | 3.98                   | 4.44                 |                      | fclII | Methylythioribose salvage protein  | +        |
| RZC03806 | BC0380 | 1.43                   | 1.41                 |                      |       | ABC transporter ATP-binding protein | -        |
| RZC02626 | BC0410 | 1.07                   | 2.91                 |                      |       | Spore coat N-acetylmuramic acid decetylase | - |
| RZC05979# | BC0593 | 8.18                   | 6.88                 |                      |       | Alanine permease                   | ‡        |
| RZC03588 | BC0632 | 2.04                   | 0.92                 |                      | treA  | Trehalose-6-phosphate hydrolase    | -        |
| RZC06568 | BC0656 | 3.42                   | 6.28                 |                      | glpT  | Glycerol-3-phosphate transporter   | 2        |
| RZC05942 | BC0661 | 2.24                   | 1.24                 |                      | rbsD  | High affinity ribose transport protein | 1        |
| RZC03214 | BC0663 | 14.56                  | 10.46                |                      | rbsC  | Ribose transport system permease protein | 2        |
| RZC03215 | BC0664 | 10.68                  | 8.44                 |                      | rbsB  | D-ribose-binding protein           | +        |
| RZC07872 | BC0754 | 4.01                   | 3.69                 |                      |       | Potassium-transporting ATPase B chain | -        |
| RZC05185 | BC0763 | 1.05                   | 3.33                 |                      |       | ABC transporter permease protein    | -        |
| RZC05182 | BC0768 | 1.37                   | 6.42                 |                      |       | Methylthioribose-binding protein   | -        |
| RZC03637 | BC0830 | 1.64                   | 3.39                 |                      |       | hypothetical protein               | -        |
| RZC03633 | BC0834 | 1.28                   | 2.79                 |                      |       | hypothetical protein               | -        |
| RZC05213 | BC0972 | 0.93                   | 4.32                 |                      |       | hypothetical protein               | 1        |
| RZC05136 | BC1053 | 2.40                   | 1.09                 |                      |       | hypothetical protein               | -        |
| RZC05869 | BC1032 | 1.26                   | 4.36                 |                      |       | Transcriptional repressor          | -        |
| RZC07888 | BC1034 | 1.41                   | 3.06                 |                      | glpF  | Glycerol uptake facilitator protein | 3        |
| RZC00019 | BC1036 | 1.53                   | 8.04                 |                      | glpD  | Glycerol-3-phosphate dehydrogenase | +        |
| RZC06104 | BC1045 | 2.27                   | 1.83                 |                      |       | hypothetical protein               | 1        |
| RZC10760 | BC1081 | 0.75                   | 15.37                |                      |       | hypothetical protein               | -        |
| RZC02201 | BC1082 | 1.54                   | 2.40                 |                      | PiCR-regulated protein Prp2  | -        |
| RZC02198 | BC1083 | 10.95                  | 8.09                 |                      |       | Ribosomal-protein-alanine acetyltransferase | 1        |
| RZC02198 | BC1083 | 10.95                  | 8.09                 |                      |       | Ribosomal-protein-alanine acetyltransferase | 1        |
| RZC07901 | BC1113 | 1.32                   | 2.23                 |                      | yhdL  | Sigma-M negative effector          | -        |
| RZC03609# | BC1149 | 2.16                   | 1.51                 |                      | rocD  | Ornithine aminotransferase         | 1        |
| RZC03622 | BC1181 | 2.07                   | 0.50                 |                      | oppC  | Oligopeptide transport system permease protein | -        |
| RZC03621 | BC1182 | 2.17                   | 0.55                 |                      | oppD  | Oligopeptide transport ATP-binding protein | -        |
| RZC06646 | BC1185 | 2.47                   | 1.38                 |                      |       | Oligopeptide-binding protein oppA  | 2        |
| RZC02368 | BC1224 | 2.16                   | 1.18                 |                      | yjcF  | Acetyltransferase                  | -        |
| RZC02369 | BC1225 | 2.92                   | 1.45                 |                      | yjcG  | 2'-5' RNA ligase                   | -        |
| RZC02366 | BC1226 | 2.50                   | 1.90                 |                      | yjcH  | Acetyl esterase                    | -        |
| RZC03344# | BC1235 | 2.18                   | 2.39                 |                      | trpC  | Indole-3-glycerol phosphate synthase | -        |
| RZC03342# | BC1237 | 2.39                   | 2.24                 |                      | trpB  | Tryptophan synthase beta chain     | -        |
| RZC036695 | BC1251 | 2.56                   | 3.97                 |                      | odhB  | Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex | +        |
| RZC06639 | BC1252 | 2.07                   | 3.80                 | 4.66                 | odhA  | 2-oxoglutarate dehydrogenase E1 component | 4        |
| RZC02375 | BC1475 | 0.86                   | 2.17                 |                      |       | ResB protein                       | -        |
| RZC02665 | BC1491 | 4.53                   | 4.74                 |                      | gudB  | NAD-specific glutamate dehydrogenase | 3        |
| RZC03717 | BC1508 | 1.83                   | 2.47                 |                      | yphF  | hypothetical protein               | -        |
| RZC03714 | BC1509 | 1.87 | 3.48 | Stage IV sporulation protein A | - |
| RZC03642 | BC1515 | 7.10 | 8.50 | Nucleoside diphosphate kinase | 1 |
| RZC035979 | BC1560 | 1.34 | 3.76 | Spore coat protein D | - |
| RZC035976 | BC1562 | 1.51 | 4.07 | ypsB Cell division protein DIVIVA | - |
| RZC01217 | BC1739 | 6.47 | 5.14 | Proton/sodium-glutamate symport protein | 1 |
| RZC07213 | BC1741 | 4.63 | 4.33 | ndS NAD-dependent malic enzyme | + |
| RZC04704# | BC1776 | 1.41 | 3.47 | Branched-chain amino acid aminotransferase | 1 |
| RZC03229# | BC1793 | 7.41 | 0.83 | Non-expressed Enterotoxin C | + |
| RZC01217 | BC1809 | 2.28 | 1.92 | nheA Non-hemolytic enterotoxin lytic component L2 | 2 |
| RZC02615 | BC1810 | 2.52 | 2.19 | nheB Non-hemolytic enterotoxin lytic component L1 | + |
| RZC00546 | BC1811 | 1.80 | 2.26 | NAD-dependent malic enzyme | 1 |
| RZC00597 | BC1821 | 3.23 | 1.61 | Pyrimidine-nucleoside phosphorylase | + |
| RZC00598# | BC1822 | 4.47 | 2.81 | Cytidine deaminase | + |
| RZC10790 | BC1919 | 1.33 | 7.74 | DNA integration/recombination/invertion protein | - |
| RZC05784 | BC1981 | 1.91 | 2.30 | Acyl carrier protein | - |
| RZC05828 | BC2018 | 1.60 | 2.32 | NarJ Respiratory nitrate reductase delta chain | - |
| RZC05831 | BC2093 | 1.56 | 3.20 | Catabolite gene activator | - |
| RZC03630 | BC2353 | 1.30 | 2.87 | YodL ABC transporter ATP-binding protein | - |
| RZC03776 | BC2519 | 1.75 | 4.32 | Lysase | - |
| RZC03776 | BC2543 | 1.30 | 2.87 | YodL ABC transporter ATP-binding protein | - |
| RZC03789 | BC2581 | 1.36 | 2.68 | Phage endonuclease | - |
| RZC05668 | BC2590 | 1.80 | 2.97 | Phage protein | - |
| RZC05831 | BC2691 | 1.76 | 3.26 | Acyl carrier protein | - |
| RZC02190 | BC2766 | 1.32 | 1.21 | acOR Sigma-54-dependent transcriptional activator | 1 |
| RZC031505 | BC3041 | 0.72 | 2.44 | ykFC Cell wall-associated hydrolase | - |
| RZC07108 | BC3093 | 1.00 | 3.25 | hypothetical protein | 1 |
| RZC05863 | BC3292 | 0.97 | 4.04 | Nucleotidyltransferase | - |
| RZC01610 | BC3296 | 1.56 | 3.20 | Sugar transport system permease protein | 1 |
| RZC06472 | BC3296 | 1.61 | 2.87 | Sugar transport system permease protein | - |
| RZC02942 | BC3296 | 1.91 | 2.64 | Sugar transport ATP-binding protein | - |
| RZC05831 | BC3296 | 1.58 | 2.39 | Sugar (pentulose and hexulose) kinases | - |
| RZC03681 | BC3296 | 2.02 | 2.53 | Polyketide synthase curC | - |
| RZC10848 | BC3310 | 0.98 | 8.71 | Microbial collagenase | 1 |
| RZC01533 | BC3341 | 2.21 | 3.80 | ywsA hypothetical protein | - |
| RZC01574 | BC3075 | 1.85 | 2.37 | ydhM EpH/GdmH-related protein | 1 |
| RZC06999 | BC3093 | 3.85 | 2.98 | Aspartate ammonia-lyase | - |
| RZC03946# | BC3189 | 1.21 | 2.07 | Serine transporter | 1 |
| RZC03586 | BC3193 | 2.45 | 3.26 | hypothetical protein | - |
| RZC10947 | BC3232 | 2.03 | 0.96 | hypothetical protein | - |
| Transcript ID | Gene ID | Description                                                                 | Function |
|--------------|---------|-------------------------------------------------------------------------------|----------|
| RZC10939     | BC3234  | Glucose/mannose transporter                                                   |          |
| RZC03663     | BC3297  | hypothetical Cytosolic Protein                                               |          |
| RZC02183     | BC3328  | ABC transporter permease protein                                             |          |
| RZC07149     | BC3345  | Collagen-like triple helix repeat protein                                     |          |
| RZC06014     | BC3446  | hypothetical protein                                                         |          |
| RZC05319     | BC3450  | hypothetical Membrane Spanning Protein                                        |          |
| RZC03190     | BC3451  | hypothetical Membrane Spanning Protein                                        |          |
| RZC03192     | BC3452  | hypothetical protein                                                         |          |
| RZC05715     | BC3477  | Quinone oxidoreductase                                                       |          |
| RZC05302     | BC3495  | glpQ Glycerophosphoryl diester phosphodiesterase                             |          |
| RZC010859    | BC3547  | Cell surface protein                                                         |          |
| RZC02909     | BC3582  | hypothetical protein                                                         |          |
| RZC01093     | BC3585  | Oligopeptide-binding protein oppA                                             |          |
| RZC04994     | BC3627  | yflS Acetyl-CoA acetyltransferase                                            |          |
| RZC013083    | BC3649  | hyster Formiminoglutamase (BC 3.5.3.8)                                       | +        |
| RZC00716#    | BC3650  | hutH Histidine ammonia-lyase                                                 |          |
| RZC00715#    | BC3651  | hutU Urocanate hydratase                                                     |          |
| RZC00321#    | BC3652  | hutH Histidine ammonia-lyase                                                 |          |
| RZC00429     | BC3681  | yneE IG hypothetical 18106                                                   |          |
| RZC00428     | BC3682  | Transketolase                                                                |          |
| RZC03035     | BC3788  | yuQ Nucleoside transport system permease protein                             |          |
| RZC00502     | BC3790  | yuO Nucleoside transport ATP-binding protein                                 |          |
| RZC00041     | BC3791  | yuN Nucleoside-binding protein                                               |          |
| RZC00040     | BC3792  | ymC Transcriptional regulator, GntR family                                  | 2        |
| RZC02281     | BC3833  | sucD Succinyl-CoA synthetase alpha chain                                      | +        |
| RZC02282     | BC3834  | sucC Succinyl-CoA synthetase beta chain                                       | 1        |
| RZC02217     | BC3921  | yhp Acetyltransferase                                                        |          |
| RZC03103     | BC3985  | hypothetical Cytosolic Protein                                               |          |
| RZC02414#    | BC4003  | metE 3-methylfurfurylerythroerythrose--homocysteine methyltransferase         |          |
| RZC06591     | BC4023  | Acetyl-CoA acetyltransferase                                                  |          |
| RZC05779     | BC4083  | Guanine-hypoxanthine permease                                                | 1        |
| RZC05592     | BC4086  | purN Purine nucleoside phosphorylase                                          |          |
| RZC01337     | BC4097  | 2.5-diketo-D-gluconic acid reductase                                          |          |
| RZC09913#    | BC4135  | L-serine dehydratase                                                         |          |
| RZC02465#    | BC4136  | L-serine dehydratase                                                         | 1        |
| RZC01173#    | BC4157  | bkdB Lipoamide acyltransferase component of branched-chain alpha-keto dehydrogenase complex | + |
| RZC05713#    | BC4158  | 2-oxosovalerate dehydrogenase beta subunit                                   |          |
| RZC01012#    | BC4159  | 2-oxosovalerate dehydrogenase alpha subunit                                  |          |
| RZC01014#    | BC4160  | lipDV Dihydrolipoamide dehydrogenase                                         |          |
| RZC02768#    | BC4161  | Branched-chain-fatty-acid kinase                                              |          |
| RZC02766#    | BC4162  | Leucine dehydrogenase                                                        | 1        |
| RZC02767#    | BC4163  | Phosphate butyryltransferase                                                  | 1        |
| RZC06622     | BC4200  | IG hypothetical 18750                                                        |          |
| RZC01281     | BC4213  | Quaternary ammonium compound-resistance protein                              |          |
| RZC00112#    | BC4224  | Glycine dehydrogenase [decarboxylating]                                      |          |
| RZC01061#    | BC4225  | Glycine dehydrogenase [decarboxylating]                                      |          |
| RZC02167#    | BC4226  | gcvT Aminomethyltransferase                                                   |          |
| RZC00730     | BC4229  | hypothetical protein                                                         | 2        |
| RZC00050     | BC4362  | Ferrichrome transport system permease protein                                 |          |
| Accession | Description                                                                 | Abundance | Fold Change |
|-----------|------------------------------------------------------------------------------|-----------|-------------|
| RZC03701 | BC4510 Sodium export ATP-binding protein                                      | 2.58      | 1.90        |
| RZC07053 | BC4516 Succinate dehydrogenase iron-sulfur protein                           | 3.76      | 5.64        |
| RZC07054 | BC4517 Succinate dehydrogenase flavoprotein subunit 1                        | 4.42      | 3.70        |
| RZC05750 | BC4518 Succinate dehydrogenase cytochrome b558 subunit 1                    | 4.35      | 4.02        |
| RZC03079 | BC4523 Electron transfer flavoprotein beta-subunit                            | 3.06      | 0.85        |
| RZC00093 | BC4524 3-hydroxybutyryl-CoA dehydrogenase                                     | 2.48      | 0.83        |
| RZC07229 | BC4583 NAD(P)-dependent glyceraldehyde-3-phosphate dehydrogenase             | 1.74      | 2.79        |
| RZC03126 | BC4592 Malate dehydrogenase                                                  | 5.81      | 4.32        |
| RZC01079 | BC4593 Isocitrate dehydrogenase [NADP]                                       | 5.56      | 4.38        |
| RZC05750 | BC4594 Succinate dehydrogenase cytochrome b558 subunit 1                    | 4.35      | 4.02        |
| RZC01149 | BC4606 hypothetical Membrane Spanning Protein                                 | 1.18      | 3.51        |
| RZC02682 | BC4642 ATP-NAD kinase                                                        | 3.92      | 1.07        |
| RZC01089 | BC4643 ABC transporter ATP-binding protein                                   | 1.57      | 4.44        |
| RZC01614 | BC4644 hypothetical Cytosolic Protein                                         | 3.33      | 2.02        |
| RZC03472 | BC5006 Prolyne dehydrogenase                                                 | 2.38      | 0.95        |
| RZC03473 | BC5009 Methyl-accepting chemotaxis protein                                    | 2.29      | 2.06        |
| RZC03473 | BC5012 Citrate synthase                                                      | 2.78      | 0.88        |
| RZC08029 | BC5131 Protein translocase subunit SecG                                       | 2.25      | 1.86        |
| RZC02760 | BC5262 Two-component response regulator                                      | 1.75      | 2.21        |
| RZC04768 | BC5297 NADH-quinone oxidoreductase chain H                                    | 2.00      | 1.35        |
| RZC00738 | BC5319 Protein tyrosine phosphatase                                           | 2.24      | 2.24        |
| RZC03472 | BC5333 Glucosamine fructose-6-phosphate aminotransferase (isomerizing)       | 3.73      | 3.34        |
| RZC03473 | BC5344 Citrate synthase                                                      | 2.73      | 2.28        |
| RZC08086 | BC5412 Two-component sensor protein yhcY                                       | 2.16      | 1.84        |
| RZC03119 | BC5439 Murein hydrolase exporter                                              | 2.11      | 6.54        |
| RZC02320 | BC5447 Acetamide transporter                                                  | 2.44      | 0.87        |
| RZC06834 | BC0189 hypothetical protein                                                   | 0.45      | 0.43        |
| RZC04620 | BC0190 Glucosamine fructose-6-phosphate aminotransferase (isomerizing)       | 0.48      | 0.66        |
| RZC03294 | BC0219 hypothetical Membrane Spanning Protein                                 | 0.45      | 0.63        |
| RZC05193 | BC0228 1-acyl-sn-glycerol-3-phosphate acyltransferase                         | 0.49      | 0.81        |
| RZC03560 | BC0253 Fumarylacetacacetase                                                   | 0.50      | 0.56        |
| RZC05027 | BC0360 Aminopeptidase                                                         | 0.69      | 0.44        |
| RZC02100 | BC0595 Cadmium efflux system accessory protein                                | 0.78      | 0.45        |
| RZC01585 | BC0612 L-lactate permease                                                     | 0.34      | 1.21        |
| RZC07860 | BC0647 RNA polymerase ECF-type sigma factor                                   | 0.86      | 0.48        |
| RZC03830 | BC0655 Universal stress protein family                                        | 0.50      | 0.85        |
| RZC05711 | BC0683 hypothetical protein                                                   | 0.96      | 0.47        |
| RZC06313 | BC0685 Branched-chain amino acid transport system carrier protein             | 0.49      | 0.50        |
| RZC00046 | BC0694 Sodium export ATP-binding protein                                      | 0.43      | 0.33        |
| RZC03841 | BC0868 NAD-dependent glyceraldehyde-3-phosphate dehydrogenase                | 0.31      | 0.26        |
| RZC03622 | BC1181 Oligopeptide transport system permease protein                         | 2.07      | 0.50        |
| RZC05965 | BC1183 Oligopeptide transport ATP-binding protein oppC                        | 1.79      | 0.48        |
| RZC00487 | BC1355 hypothetical protein                                                   | 0.57      | 0.76        |
| RZC03432 | BC1908 hypothetical protein                                                   | 0.54      | 0.36        |
| RZC05932 | BC1924 L-lactate dehydrogenase                                                | 0.44      | 1.05        |
| RZC00144 | BC2035 Magnesium and cobalt transport protein corA                             | 0.38      | 0.74        |
| Accession  | BC     | F1   | F2   | Gene/Protein                                                                 |
|------------|--------|------|------|------------------------------------------------------------------------------|
| RZC00219  | BC2121 | 0.53 | 0.49 | narI  Respiratory nitrate reductase gamma chain                              |
| RZC01018  | BC2369 | 0.47 | 0.46 | Acetyltransferase                                                            |
| RZC08307  | BC2453 | 0.55 | 0.44 | ppsC  Peptide synthetase                                                     |
| RZC00208  | BC2771 | 0.36 | 0.58 | hypothetical protein                                                         |
| RZC00218  | BC2795 | 0.29 | 0.35 | Ferredoxin                                                                   |
| RZC05794  | BC3221 | 0.46 | 0.87 | surface protein                                                              |
| RZC02185  | BC3329 | 0.91 | 0.31 | ABC transporter ATP-binding protein                                           |
| RZC06783  | BC3557 | 1.49 | 0.24 | sqhC  Squalene—hopene cyclase                                                |
| RZC06776  | BC3595 | 0.66 | 0.45 | yvaA  Oxidoreductase                                                         |
| RZC01178  | BC3720 | 0.51 | 0.73 | fruR  Fructose repressor                                                    |
| RZC00386  | BC3848 | 0.39 | 1.02 | acpA  Acyl carrier protein                                                  |
| RZC06588  | BC3857 | 1.17 | 0.12 | yloS  Thiamin pyrophosphokinase                                              |
| RZC06584  | BC3859 | 1.32 | 0.44 | hypothetical Membrane Spanning Protein                                       |
| RZC06581  | BC3880 | 1.23 | 0.48 | hypothetical Membrane Spanning Protein                                       |
| RZC02045  | BC3883 | 0.83 | 0.19 | pyrF  Orotidine 5'-phosphate decarboxylase                                  |
| RZC02044  | BC3884 | 0.88 | 0.20 | pyrD  Dihydroorotate dehydrogenase, catalytic subunit                        |
| RZC06579  | BC3885 | 1.02 | 0.14 | pyrK  Dihydroorotate dehydrogenase electron transfer subunit                 |
| RZC06578  | BC3886 | 1.04 | 0.11 | hypothetical protein                                                         |
| RZC02045  | BC3887 | 1.14 | 0.33 | pyrC  Dihydroorotase                                                        |
| RZC05814  | BC3889 | 0.75 | 0.30 | hypothetical Membrane Spanning Protein                                       |
| RZC05813  | BC3890 | 0.69 | 0.25 | pyrP  Uracil permease                                                        |
| RZC06068  | BC3931 | 0.42 | 1.06 | hypothetical protein                                                         |
| RZC02185  | BC3996 | 0.18 | 0.58 | hypothetical protein                                                         |
| RZC02185  | BC4017 | 0.52 | 0.30 | 3-oxoacyl-[acyl-carrier protein] reductase                                    |
| RZC05706  | BC4088 | 0.45 | 1.09 | hypothetical protein                                                         |
| RZC00154  | BC4240 | 0.27 | 1.02 | hypothetical protein                                                         |
| RZC05291  | BC4259 | 0.74 | 0.45 | hypothetical protein                                                         |
| RZC05299  | BC4599 | 0.29 | 0.33 | Pyruvate kinase                                                             |
| RZC02283  | BC4600 | 0.45 | 0.47 | hypothetical protein                                                         |
| RZC00434  | BC4658 | 0.29 | 0.60 | hypothetical protein                                                         |
| RZC034869 | BC4669 | 0.47 | 0.54 | hypothetical protein                                                         |
| RZC03693  | BC4766 | 0.30 | 0.26 | hypothetical protein                                                         |
| RZC03793  | BC4898 | 0.31 | 0.20 | hypothetical protein                                                         |
| RZC05291  | BC5018 | 0.46 | 0.58 | hypothetical Membrane Spanning Protein                                       |
| RZC05299  | BC5026 | 0.50 | 1.11 | hypothetical protein                                                         |
| RZC06290  | BC5051 | 0.93 | 0.41 | ALS Sodium/proton-dependent alanine carrier protein                           |
| RZC05504  | BC5116 | 0.44 | 0.81 | hypothetical protein                                                         |
| RZC05498  | BC5117 | 0.67 | 0.47 | hypothetical protein                                                         |
| RZC05499  | BC5118 | 0.76 | 0.48 | hypothetical protein                                                         |
| RZC05500  | BC5119 | 0.68 | 0.45 | hypothetical protein                                                         |
| RZC05497  | BC5121 | 0.67 | 0.48 | hypothetical protein                                                         |
| RZC05494  | BC5122 | 0.68 | 0.49 | hypothetical protein                                                         |
| RZC05501  | BC5123 | 0.69 | 0.48 | hypothetical protein                                                         |
| RZC05490  | BC5124 | 0.66 | 0.48 | hypothetical protein                                                         |
| RZC05496  | BC5125 | 0.68 | 0.42 | hypothetical protein                                                         |
| RZC02971  | BC5135 | 0.42 | 0.51 | hypothetical protein                                                         |
| RZC05843  | BC5136 | 0.48 | 0.38 | hypothetical protein                                                         |
| RZC07010  | BC5137 | 0.50 | 0.41 | hypothetical protein                                                         |
| RZC08031  | BC5138 | 0.53 | 0.46 | hypothetical protein                                                         |
| RZC00211  | BC5139 | 0.49 | 0.41 | hypothetical protein                                                         |
| RZC00210  | BC5140 | 0.36 | 0.59 | hypothetical protein                                                         |
| RZC08032  | BC5141 | 0.49 | 0.73 | hypothetical protein                                                         |

- = not applicable
| Gene ID   | Accession | Expression Ratio (Early) | Expression Ratio (Mid) | Function                                                                 |
|----------|-----------|--------------------------|------------------------|--------------------------------------------------------------------------|
| RZC00782 | BC5320    | 0.32                     | 0.24                   | ypqE, PTS system, glucose-specific IIA component                         |
| RZC03557 | BC5335    | 0.39                     | 0.52                   | fbaA, Fructose-bisphosphate aldolase                                     |
| RZC05846 | BC5359    | 0.45                     | 0.47                   | ywaD, Aminopeptidase Y                                                  |
| RZC01390 | BC5368    | 0.38                     | 0.27                   | Transcriptional regulator pfoR                                           |
| RZC05205 | BC5380    | 0.46                     | 0.52                   | ywaD, Aminopeptidase Y                                                  |
| RZC04933 | BC5396    | 0.49                     | 0.44                   | yxeH, Hydrolase (HAD superfamily)                                        |

* Expression ratio’s are presented as in the ccpA deletion strain compared to the wild type, wild type expression is set to 1. Early-exponential is sampled at an OD<sub>600</sub> of 0.2 and mid-exponential at 0.8.
† Expression ratio’s of qPCR are presented as in the ccpA deletion strain compared to the wild type, gene expression is related to the household gene rpoA.
‡ In this column it is indicated whether a putative CRE-site was identified for the gene. Numbers indicate the number of putative CRE-sites identified, a + indicates that a gene is in the same operon as a gene for which a putative CRE-site was identified, and a – indicates no putative CRE-site could be identified.
§ Possibly in operon with gene for which a CRE-site was identified, however this gene was absent from the microarray.
# Genes, higher expressed in the ccpA deletion strain, with an apparent putative function in protein, peptide or amino acid metabolism.