Table S1 Detailed information of 53 *R. equi* genomes.

| No. | Strain     | Size (Mb) | G+C (mol%) | CDS | tRNA | rRNA | tmRNA | Level     | Accession No.         | Plasmid type | Plasmid accession No. |
|-----|------------|-----------|------------|-----|------|------|-------|-----------|----------------------|--------------|-----------------------|
| 1   | CHPC 1.8375 | 5.13      | 68.52      | 4778| 61   | 7    |       | 1 Contig  | JAJENO0000000000001 | VAPB         |                       |
| 2   | CHPC 1.8376 | 5.26      | 68.61      | 4937| 66   | 8    |       | 1 Contig  | JAJENN0000000000001 | VAPB         |                       |
| 3   | CHPC 1.8383 | 5.08      | 68.57      | 4710| 60   | 8    |       | 1 Contig  | JAJENL0000000000001 | VAPB         |                       |
| 4   | CHPC 1.8384 | 5.16      | 68.56      | 4796| 61   | 3    |       | 1 Contig  | JAJENL0000000000001 | VAPB         |                       |
| 5   | 103S       | 5.04      | 68.8       | 4582| 63   | 12   |       | 1 Complete| GCA_000196695.1     | VAPA         | NC_011151.1           |
| 6   | ATCC 13557 | 5.29      | 68.5       | 4563| 66   | 5    |       | 1 Complete| GCA_016921075.1     | -            | -                     |
| 7   | ATCC 33707 | 5.26      | 68.75      | 4898| 64   | 15   |       | 1 Contig  | GCA_000164155.2     | -            | -                     |
| 8   | C 7        | 5.2       | 68.8       | 4742| 62   | 3    | NA    | Contig    | GCA_000473915.1     | -            | -                     |
| 9   | DE0411     | 5.27      | 68.8       | 4819| 63   | 3    |       | 1 Scaffold| GCA_007672705.1     | -            | -                     |
| 10  | DSM 20307  | 5.2       | 68.8       | 4772| 64   | 3    |       | 1 Contig  | GCA_002094305.1     | -            | -                     |
| 11  | DSSKP-R-001| 5.44      | 68.66      | 5055| 75   | 15   |       | 1 Complete| GCA_003013675.1     | -            | -                     |
| 12  | FDAARGOS_952| 5.22     | 68.8       | 4768| 63   | 12   |       | 1 Complete| GCA_016025875.1     | -            | -                     |
| 13  | N1288      | 5.17      | 68.8       | 4737| 59   | 3    |       | 1 Contig  | GCA_001646885.1     | -            | -                     |
| 14  | N1295      | 5.31      | 68.7       | 4869| 64   | 3    |       | 1 Contig  | GCA_001646905.1     | -            | -                     |
| 15  | N1301      | 5.65      | 68.5       | 5179| 60   | 3    |       | 1 Contig  | GCA_001646925.1     | -            | -                     |
| 16  | NBRC 101255| 5.2       | 68.8       | 4771| 63   | 3    |       | 1 Contig  | GCA_001552575.1     | -            | -                     |
| 17  | NCTC1621   | 5.24      | 68.8       | 4783| 64   | 12   |       | 2 Contig  | GCA_900455845.1     | -            | -                     |
| 18  | NCTC5650   | 5.31      | 68.7       | 4820| 63   | 12   |       | 1 Contig  | GCA_900455885.1     | -            | -                     |
| 19  | PAM1204    | 5.23      | 68.8       | 4773| 61   | 3    |       | 1 Contig  | GCA_002078545.1     | VAPN         | NZ_KX443398.1         |
| 20  | PAM1216    | 5.2       | 68.8       | 4772| 67   | 3    |       | 1 Contig  | GCA_002095175.1     | VAPA         | NZ_KX443388.1         |
| 21  | PAM1271    | 5.2       | 68.8       | 4780| 66   | 3    |       | 1 Contig  | GCA_002095045.1     | VAPA         | NZ_KX443396.1         |
|   | Description | Bit Score | E Value | Length | Identity | Contig ID | Accession ID | Accession Description |
|---|-------------|-----------|---------|--------|----------|-----------|--------------|-----------------------|
| 22 | PAM1340     | 5.06      | 68.8    | 4633   | 61       | 1          | Contig_GCA_002095085.1 VAPA | NZ_KX443392.1          |
| 23 | PAM1354     | 5.37      | 68.8    | 4919   | 67       | 1          | Contig_GCA_002095035.1 VAPN | NZ_KX443399.1          |
| 24 | PAM1357     | 5.01      | 68.8    | 4578   | 63       | 1          | Contig_GCA_002095125.1 VAPA | NZ_KX443389.1          |
| 25 | PAM1413     | 5.04      | 68.8    | 4606   | 64       | 1          | Contig_GCA_002095115.1 VAPB | NZ_KX443406.1          |
| 26 | PAM1422     | 5.2       | 68.8    | 4780   | 64       | 1          | Contig_GCA_002095195.1 VAPA | NZ_KX443390.1          |
| 27 | PAM1475     | 5.21      | 68.8    | 4768   | 63       | 4          | Contig_GCA_002095185.1 VAPB | NZ_KX443397.1          |
| 28 | PAM1496     | 5.08      | 68.8    | 4780   | 64       | 3          | Contig_GCA_002095155.1 VAPA |              |
| 29 | PAM1533     | 5.13      | 68.8    | 4722   | 62       | 3          | Contig_GCA_002095235.1 VAPB | NZ_KX443407.1          |
| 30 | PAM1557     | 5.35      | 68.8    | 4908   | 69       | 3          | Contig_GCA_002095255.1 VAPN | NZ_KX443400.1          |
| 31 | PAM1571     | 5.42      | 68.8    | 4951   | 65       | 3          | Contig_GCA_002094265.1 VAPN | NZ_KF439868.1          |
| 32 | PAM1572     | 5.12      | 68.8    | 4669   | 61       | 3          | Contig_GCA_002078535.1 VAPN | NZ_KX443401.1          |
| 33 | PAM1593     | 5.24      | 68.8    | 4807   | 62       | 3          | Contig_GCA_002078625.1 VAPB | NC_011150.1            |
| 34 | PAM1600     | 5.14      | 68.8    | 4703   | 59       | 3          | Contig_GCA_002078515.1 VAPB | NZ_KX443391.1          |
| 35 | PAM1637     | 5.08      | 68.8    | 4634   | 66       | 3          | Contig_GCA_002095295.1 VAPA | NZ_KX443393.1          |
| 36 | PAM1643     | 5.09      | 68.8    | 4691   | 62       | 3          | Contig_GCA_002094235.1 VAPA | NZ_KX443394.1          |
| 37 | PAM2012     | 5.33      | 68.7    | 4877   | 66       | 3          | Contig_GCA_002094445.1 VAPN | NZ_KP851975.1          |
| 38 | PAM2274     | 5.22      | 68.7    | 4812   | 60       | 3          | Contig_GCA_002094225.1 - | -                     |
| 39 | PAM2279     | 5.03      | 68.8    | 4619   | 61       | 3          | Contig_GCA_002094375.1 VAPB | NZ_KX443405.1          |
| 40 | PAM2282     | 5.27      | 68.7    | 4831   | 63       | 3          | Contig_GCA_002094295.1 VAPA | NZ_KX443395.1          |
| 41 | PAM2285     | 5.19      | 68.8    | 4746   | 64       | 3          | Contig_GCA_002094395.1 VAPA | NZ_KX443402.1          |
| 42 | PAM2287     | 5.14      | 68.9    | 4684   | 63       | 3          | Contig_GCA_002094405.1 VAPA | NZ_KX443404.1          |
| 43 | PAM2288     | 5.48      | 68.7    | 5081   | 65       | 3          | Contig_GCA_002094325.1 VAPA | NZ_KX443403.1          |
| 44 | PAM2289     | 5.35      | 68.7    | 4916   | 62       | 3          | Contig_GCA_017116975.1 - | -                     |
| 45 | PAM2291     | 5.47      | 68.7    | 5040   | 62       | 3          | Contig_GCA_017117025.1 - | -                     |
| 46 | PAM2292     | 5.45      | 68.6    | 5071   | 66       | 3          | Contig_GCA_017117065.1 - | -                     |
| 47 | PAM2293     | 5.4       | 68.7    | 4999   | 65       | 3          | Contig_GCA_017117085.1 - | -                     |
Table S2 Detailed information of 33 R. genome.

| No. | Organism Name         | Strain     | Size(Mb) | G+C(mol%) | Level    | Accession No.          |
|-----|-----------------------|------------|----------|-----------|----------|------------------------|
| 1   | R.aetherivorans       | BCP1       | 6.23     | 70.34     | complete | GCA_000470885.1        |
| 2   | R.agglutinans         | CCTCCAB2014297 | 5.43     | 69.2      | contig   | GCA_004011865.1        |
| 3   | R.biphenylivorans     | TG9        | 5.03     | 68        | complete | GCA_003288095.1        |
| 4   | R.coprophilus         | NCTC10994 | 4.58     | 66.8      | complete | GCA_900478115.1        |
| 5   | R.corynebacterioides  | NBRC14404 | 3.97737  | 70.3      | contig   | GCA_001894765.1        |
| 6   | R.encensis            | NIO-1009   | 7.47874  | 62.3      | scaffold | GCA_900094765.1        |
| 7   | R.erythropolis        | NCTC8036   | 6.55124  | 62.4      | contig   | GCA_900455855.1        |
| 8   | R.fascians            | D188       | 5.50211  | 64.584    | complete | GCA_001620305.1        |
| 9   | R.globerulas          | WS3306     | 6.77108  | 61.7      | contig   | GCA_003097035.1        |
| 10  | R.gordonae            | NCTC13296  | 4.87192  | 67.9      | contig   | GCA_900455725.1        |
| 11  | R.hoagii              | DSSKP-R-001 | 5.43883  | 68.6647   | complete | GCA_003013675.1        |
| 12  | R.imtechensis         | RKJ300     | 8.23134  | 67.2      | contig   | GCA_000260815.1        |
| 13  | R.jostii              | DSM44719   | 9.91298  | 66.9      | contig   | GCA_900105375.1        |
| 14  | R.koreensis           | DSM44498   | 10.3116  | 67.4      | contig   | GCA_900105905.1        |
| 15  | R.kroppenstedtii      | DSM44908   | 4.08283  | 70.1      | contig   | GCA_900111805.1        |
| 16  | R.kyotonensis         | JCM23211   | 6.31101  | 64.2      | scaffold | GCA_900188125.1        |
| No. | Name                  | Gene     | NO.of Strain | Drug Class       | Identity of Matching Region | Coverage of Reference Sequence % |
|-----|-----------------------|----------|--------------|------------------|-------------------------------|---------------------------------|
| 17  | *R. maanshanensis*    |          | 5.67371      | 69.2             | contig                        | GCA_001894865.1                 |
| 18  | *R. marinonascens*    |          | 4.92         | 64.4             | contig                        | GCA_001894885.1                 |
| 19  | *R. opacus*           |          | 8.84147      | 67.1027          | complete                      | GCA_019856255.1                 |
| 20  | *R. oryzae*           |          | 5.37         | 69.2             | contig                        | GCA_005049235.1                 |
| 21  | *R. percolatus*       |          | 7.88481      | 67.4             | contig                        | GCA_017875695.1                 |
| 22  | *R. pyridinivorans*   |          | 5.26248      | 67.8             | contig                        | GCA_001015195.1                 |
| 23  | *R. qingshengii*      |          | 6.72611      | 62.3484          | complete                      | GCA_015099595.1                 |
| 24  | *R. rhodnii*          |          | 4.4918       | 69.6             | scaffold                      | GCA_008011915.1                 |
| 25  | *R. rhodochrous*      |          | 5.27476      | 68.2             | complete                      | GCA_00187265.1                  |
| 26  | *R. ruber*            |          | 5.36661      | 70.6             | complete                      | GCA_001427765.1                 |
| 27  | *R. subtropicus*      |          | 4.4          | 69.1             | scaffold                      | GCA_005434945.1                 |
| 28  | *R. triatomae*        |          | 4.77616      | 68.7             | complete                      | GCA_014217765.1                 |
| 29  | *R. trifolii*         |          | 5.29         | 65.5             | contig                        | GCA_014635345.1                 |
| 30  | *R. tuksamuensis*     |          | 5.48901      | 69.8             | contig                        | GCA_00101735.1                  |
| 31  | *R. wratislaviensis*  |          | 7.83569      | 67.4             | contig                        | GCA_003385055.1                 |
| 32  | *R. yunnanensis*      |          | 6.37         | 63.9             | contig                        | GCA_001895005.1                 |
| 33  | *R. zopffii*          |          | 6.29721      | 68.2             | contig                        | GCA_001895025.1                 |

Table S3 Antimicrobial resistance gene of *Rhodococcus*
| Species                  | Protein | Resistance Type                                                                 | Resistance Value | Sensitivity |
|-------------------------|---------|---------------------------------------------------------------------------------|------------------|-------------|
| *R. corynebacterioides* | RbpA    | rifamycin antibiotic                                                             | 86.73            | 100         |
| *R. enclensis*          | RbpA    | rifamycin antibiotic                                                             | 86.49            | 98.25       |
|                         |         | Trimethoprim-resistant dihydrofolate reductase DfrA43                           | 39.71            | 83.59       |
|                         | *iri*   | rifamycin antibiotic                                                             | 95.79            | 99.79       |
| *Mycobacterium tuberculosi* nov *, foIC with mutation conferring resistance to para-aminosalicylic acid | | | 67.77 | 98.36 |
| *R. erythropolis*       | *iri*   | rifamycin antibiotic                                                             | 96.19            | 99.16       |
|                         | RbpA    | rifamycin antibiotic                                                             | 85.59            | 98.25       |
|                         |         | *Mycobacterium tuberculosi* nov *, foIC with mutation conferring resistance to para-aminosalicylic acid | 67.77 | 98.36 |
| *R. erythrops* D188     |         | antibiotic target protection                                                     | 98.25            |             |
| *R. globerulus*         | RbpA    | rifamycin antibiotic                                                             | 86.49            | 98.25       |
|                         |         | Trimethoprim-resistant dihydrofolate reductase DfrA43                           | 40.14            | 83.59       |
| *Mycobacterium tuberculosi* nov *, foIC with mutation conferring resistance to para-aminosalicylic acid | | | 67.63 | 99.38 |
| *R. gordoniae*          | RbpA    | rifamycin antibiotic                                                             | 89.19            | 98.25       |
| *R. intechensis RKJ300* | RbpA    | rifamycin antibiotic                                                             | 88.29            | 98.25       |
| *Mycobacterium tuberculosi* nov *, foIC with mutation conferring resistance to para-aminosalicylic acid | | | 68.72 | 97.54 |
| *R. jostii*             | RbpA    | rifamycin antibiotic                                                             | 87.39            | 98.25       |
| *R. koreensis*          | Trimethoprim-resistant dihydrofolate reductase DfrA43                           | 33.72            | 83.59       |
| Organism                  | Gene | Antibiotic Type                                      | MIC (μg/mL) | Zone (mm) |
|--------------------------|------|-----------------------------------------------------|-------------|-----------|
| *R. kroppenstedtii*       | *RbpA* | rifamycin antibiotic                               | 87.61       | 100       |
| *R. kyotonensis*          | *RbpA* | rifamycin antibiotic                               | 90.09       | 98.25     |
| *R. maanshanensis*        | *RbpA* | rifamycin antibiotic                               | 88.29       | 98.25     |
| *R. marinonascens*        | *RbpA* | rifamycin antibiotic                               | 87.39       | 98.25     |
| *M. tuberculosis*         | *folC* | para-aminosalicylic acid                           | 66.6        | 97.54     |
| *R. opacus*               |       | Trimethoprim-resistant dihydrofolate reductase DfrA43 | 33.72       | 86.15     |
| *R. oryzae*               |       | Trimethoprim-resistant dihydrofolate reductase DfrA43 | 37.72       | 82.56     |
| *R. percolatus*           | *RbpA* | rifamycin antibiotic                               | 88.29       | 98.25     |
|                          |       | Trimethoprim-resistant dihydrofolate reductase DfrA43 | 33.72       | 86.15     |
| Bacterial Strain | Protein/Enzyme | Antibiotic Sensitivity | % Sensitivity 1 | % Sensitivity 2 |
|-----------------|---------------|------------------------|----------------|----------------|
| *Mycobacterium tuberculosis* folC with mutation conferring resistance to para-aminosalicylic acid | RbpA | rifamycin antibiotic | 68.72 | 97.54 |
| R. *pyridinivorans* | RbpA | rifamycin antibiotic | 89.19 | 98.25 |
| R. *qingshengii* | RbpA | rifamycin antibiotic | 86.49 | 98.25 |
| *Mycobacterium tuberculosis* folC with mutation conferring resistance to para-aminosalicylic acid | RbpA | rifamycin antibiotic | 67.77 | 98.36 |
| R. *rhodnii* | RbpA | rifamycin antibiotic | 85.59 | 98.25 |
| R. *rhodochrous* | RbpA | rifamycin antibiotic | 88.29 | 98.25 |
| R. *rubner* | Trimethoprim-resistant dihydrofolate reductase DfrA43 | Diaminopyrimidine antibiotic | 33.15 | 84.62 |
| RbpA | rifamycin antibiotic | 84.68 | 98.25 |
| R. *sp. BCP1* | Trimethoprim-resistant dihydrofolate reductase DfrA43 | Diaminopyrimidine antibiotic | 32.02 | 84.62 |
| RbpA | rifamycin antibiotic | 84.68 | 98.25 |
| R. *subtropicus* | RbpA | rifamycin antibiotic | 88.29 | 98.25 |
| R. *triatomae* | RbpA | rifamycin antibiotic | 87.39 | 98.25 |
| R. *trifolii* | RbpA | rifamycin antibiotic | 87.72 | 100 |
| R. *tukisamuensis* | RbpA | rifamycin antibiotic | 88.29 | 98.25 |
| R. *wratislaviensis* | RbpA | rifamycin antibiotic | 32.74 | 86.15 |
| Trimethoprim-resistant dihydrofolate reductase DfrA43 | RbpA | rifamycin antibiotic | 68.72 | 97.54 |
| *Mycobacterium tuberculosis* folC with mutation conferring resistance to para-aminosalicylic acid | RbpA | rifamycin antibiotic | 88.29 | 98.25 |
| R. *yunnanensis* | RbpA | rifamycin antibiotic | 86.49 | 98.25 |
| R. *zopfii* | RbpA | rifamycin antibiotic | 86.49 | 98.25 |
### Table S4 The virulence factors of *R. equi*.

| VFclass      | Virulence factors                                                                 | Related genes |
|--------------|-----------------------------------------------------------------------------------|---------------|
| Adherence    | GroEL (*Clostridium*)                                                             | groEL         |
|              | Streptococcal plasmin receptor/GAPDH (*Streptococcus*)                             | plr/gapA      |
|              | The tad locus (*Haemophilus*)                                                      | tadA          |
|              | ABC transporter                                                                    | fagA          |
|              |                                                                                  | fagB          |
|              |                                                                                  | fagC          |
|              |                                                                                  | fagD          |
|              |                                                                                  | hmuU          |
|              |                                                                                  | hmuV          |
| Iron uptake  | Exochelin (*smegmatis*) (*Mycobacterium*)                                          | exiT          |
|              |                                                                                  | fxbA          |
|              | Heme uptake (*Mycobacterium*)                                                     | mmpL3         |
|              | Mycobactin (*Mycobacterium*)                                                      | fadD33        |
|              |                                                                                  | fadE14        |
|              |                                                                                  | mbtH          |
|              |                                                                                  | mbtI          |
| Regulation   | Diphtheria toxin repressor DtxR                                                   | dtxR          |
|              | (p)ppGpp synthesis and hydrolysis (*Mycobacterium*)                                | relA          |
|              | DevR/S (*Mycobacterium*)                                                          | devR/dosR     |
|              | MprA/B (*Mycobacterium*)                                                          | mprB          |
|              | PhoP/R (*Mycobacterium*)                                                          | phoP          |
|              | PrrA/B (*Mycobacterium*)                                                          | prrA/B
| Category                          | Gene Product                        | Abbreviation |
|----------------------------------|-------------------------------------|--------------|
| SenX3 (Mycobacterium)            | senX3                               |              |
| Sigma A (Mycobacterium)          | sigA/rpoV                           |              |
| Sigma D (Mycobacterium)          | sigD                                |              |
| Sigma E (Mycobacterium)          | sigE                                |              |
| Sigma F (Mycobacterium)          | sigF                                |              |
| Sigma M (Mycobacterium)          | sigM                                |              |
| WhiB3 (Mycobacterium)            | whiB3                               |              |
| Toxin                            | Phospholipase D                     | pld          |
| Acid resistance                  | Urease (Helicobacter)               | ureB         |
|                                  |                                     | ureG         |
| Amino acid and purine metabolism | Glutamine synthesis (Mycobacterium) | glnA1        |
|                                  | Lysine synthesis (Mycobacterium)    | lysA         |
|                                  | Proline synthesis (Mycobacterium)   | proC         |
|                                  | Purine synthesis (Mycobacterium)    | purC         |
|                                  | Tryptophan synthesis (Mycobacterium)| trpD         |
| Anaerobic respiration            | Nitrate reductase (Mycobacterium)   | narG         |
|                                  |                                     | narH         |
|                                  |                                     | narI         |
|                                  | Nitrate/nitrite transporter (Mycobacterium) | narK2       |
| Anti-apoptosis factor            | NuoG (Mycobacterium)               | nuoG         |
| Catabolism of cholesterol        | Cyp125 (Mycobacterium)             | cyp125       |
|                                  | FadE28 (Mycobacterium)             | fadE28       |
|                                  | FadE29 (Mycobacterium)             | fadE29       |
|                                  | Carboxylesterase (Mycobacterium)    | caeA         |
| Cell surface components          | GPL locus (Mycobacterium)           | Rx0926       |
|                                  |                                     | fadE5        |
| Function                                    | Category                                                                 | Genes |
|---------------------------------------------|---------------------------------------------------------------------------|-------|
| PDIM (phthiocerol dimycocerosate) and PGL (phenolic glycolipid) biosynthesis and transport | Mycobacterium                                                              |       |
| Trehalose-recycling ABC transporter         | Mycobacterium                                                              |       |
| Copper uptake                               | Copper exporter (Mycobacterium)                                           |       |
| Immune evasion                              | Capsule (Streptococcus)                                                   |       |
| Immune evasion                              | Exopolysaccharide (Haemophilus)                                           |       |
| Immune evasion                              | Polysaccharide capsule (Bacillus)                                         |       |
| Iron acquisition                            | Bacillibactin (Bacillus)                                                  |       |
| Lipid and fatty acid metabolism             | FAS-II (Mycobacterium)                                                    |       |
| Lipid and fatty acid metabolism             | Isocitrate lyase (Mycobacterium)                                         |       |
| Lipid and fatty acid metabolism             | Pantothenate synthesis (Mycobacterium)                                   |       |
| Mammalian cell entry (mce) operons          | Mce                                                                       |       |
| Mammalian cell entry (mce) operons          | mce3E/mce4B                                                               |       |
| Others                                      | O-antigen (Yersinia)                                                      |       |
| Others                                      | WcaG                                                                      |       |
| Others                                      | Nucleoside diphosphate kinase (Mycobacterium)                            |       |
| Others                                      | Tyrosine phosphatase (Mycobacterium)                                     |       |
| Others                                      | Proteasome-associated proteins (Mycobacterium)                           |       |
| Others                                      | Zn++ metallophrotease (Mycobacterium)                                    |       |
| Secreted proteins                           | Alpha-crystallin (Mycobacterium)                                          |       |
| Secreted proteins                           | Enhanced intracellular survival protein (Mycobacterium)                  |       |
| Secreted proteins                           | Protein kinase G (Mycobacterium)                                         |       |

| Genes | Description                                      |
|-------|--------------------------------------------------|
| rmlA  | MymA operon (Mycobacterium)                      |
| adhD  | MymA                                             |
| mymA  | sadH                                             |
| ddrA  | PDIM (phthiocerol dimycocerosate) and PGL (phenolic glycolipid) biosynthesis and transport (Mycobacterium) |
| sugC  | Trehalose-recycling ABC transporter (Mycobacterium) |
| ctpV  | Copper exporter (Mycobacterium)                  |
| rmlB/rfbB-I | Copper uptake (Mycobacterium)              |
| pgi   | Capsule (Streptococcus)                         |
| galE  | Exopolysaccharide (Haemophilus)                 |
| dhbA/E| Polysaccharide capsule (Bacillus)               |
| kasB  | FAS-II (Mycobacterium)                          |
| icl   | Isocitrate lyase (Mycobacterium)                |
| panC  | Pantothenate synthesis (Mycobacterium)          |
| panD  |                                                  |
| mce3E/mce4B | Mammalian cell entry (mce) operons          |
| wcaG  |                                                  |
| ndk   | Nucleoside diphosphate kinase (Mycobacterium)  |
| ptpA  | Tyrosine phosphatase (Mycobacterium)            |
| mpa   | Proteasome-associated proteins (Mycobacterium)  |
| pafA  |                                                  |
| zmp1  | Zn++ metallophrotease (Mycobacterium)           |
| hspX  | Secreted proteins (Mycobacterium)               |
| eis   |                                                  |
| pknG  |                                                  |
| Secretion system | ESX-1 (T7SS) (*Mycobacterium*) | espR |
|------------------|--------------------------------|------|
|                  | ESX-4 (T7SS) (*Mycobacterium*) | eccC4|
|                  |                                | mycP4|
| Stress adaptation| Catalase (*Neisseria*)         | katA |
|                  | Cu                             | sodC |
|                  | Iron-cofactored SOD (*Mycobacterium*) | sodA |