Table S3. Classification of the genes uniquely induced or repressed in *M. tuberculosis* grown under hypoxic, starvation, acidic or stationary phase condition compared to exponential growth condition. In parenthesis is given the percentage relative to the total number of genes in the *M. tuberculosis* genome in each category.

| Functional category                  | Hypoxic | Starvation | Acidic | Stationary phase |
|--------------------------------------|---------|------------|--------|------------------|
| log2 fold change                     | > 2     | < -2       | > 2    | < -2             | > 2    | < -2 |
| virulence, detoxification, adaptation| 27 (12) | 10 (4)     | 3 (1)  | 15 (6)           | 0 (0)  | 1 (0) |
| lipid metabolism                     | 30 (12) | 10 (4)     | 12 (5) | 16 (7)           | 2 (1)  | 1 (0) |
| information pathways                 | 10 (4)  | 14 (6)     | 10 (4) | 17 (7)           | 0 (0)  | 1 (0) |
| cell wall and cell processes         | 55 (7)  | 52 (7)     | 43 (6) | 36 (5)           | 4 (1)  | 2 (0) |
| insertion seqs and phages            | 11 (7)  | 3 (2)      | 3 (2)  | 2 (1)            | 0 (0)  | 3 (2) |
| PE/PPE                               | 22 (13) | 1 (1)      | 8 (5)  | 2 (1)            | 1 (1)  | 1 (1) |
| intermediary metabolism and respiration | 80 (9) | 37 (4)     | 24 (3) | 91 (10)          | 3 (0)  | 1 (0) |
| regulatory proteins                  | 14 (7)  | 6 (3)      | 16 (8) | 8 (4)            | 0 (0)  | 0 (0) |
| conserved hypotheticals              | 39 (4)  | 76 (7)     | 78 (7) | 49 (4)           | 2 (0)  | 4 (0) |

