

## Supporting Online Material for

# ***Mycobacterium avium* subsp. *paratuberculosis* induces differential cytosine methylation at miR-21 transcription start site region**

**Mostoufi-Afshar, S.; Tabatabaei, M. and Ghahramani Seno, M. M.\***

\*To whom correspondence should be addressed: E-mail: [mgseno@um.ac.ir](mailto:mgseno@um.ac.ir)

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### **This PDF file includes:**

Supplementary Tables (ST1 to ST3)

### **Supplementary Tables**

**ST1:** The sequence of the region at miR-21 TSS corresponding to the large segment analysed for differential methylation in this work

**ST2:** List of the predicted transcription factor binding sites occurring at miR-21 TSS. The genomic region corresponding to the large segment analysed for differential methylation in this work was used for the analysis using Promo software (Messegueur *et al.*, 2002; Farré *et al.*, 2003)

**ST3:** List of the predicted transcription factor binding sites known to control autophagy (Füllgrabe *et al.*, 2016) occurring at miR-21 TSS. The genomic region corresponding the large segment analysed for differential methylation in this work was used for the analysis using Promo software (Messegueur *et al.*, 2002; Farré *et al.*, 2003)

**ST1:** The sequence of the region at miR-21 TSS corresponding to the large segment analysed for differential methylation in this work

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**TATGCTCTACTGGGAAATTTGTCTTTGTCTTAGACTAGAAAGTGAACCTCTGTACATCTTCTCTCTAAAAACAAGGGTAGAGCCAATGGAAAGTAATGGTTCTGTTACATAGAATGAGTTGTTGCCTTGATCTTAAATGATGTATTGGTAGATATACTTCCCAAGTGGATTAAAAAGTTAAAACCTACAGCATAACAAAGTATTAGACTTACTGAGGTGACTTGAATATCTCCTTTTGATTTTCACTCTATTTTCTTTTCACCCATGGGAAAATGATAATTTTAAATAAACCAAGGCTCTTACCATAGCTGAACCTTAAAACCTAGACTGTCTTTCTGTAAACGATTCTGAGGCCAAAGGAAATGACTAGAAGAGGATGAGTAAACAATAACCTGAAATGGGAAACTCGAGGGAAGCACAGGTTTTTTTTGTTTTTTTTTGTTGGTTGTTTTTTGTTCTTTGGGTTTTTTTTGAGACAGAATTTTCGCTCTCGTTGCCCAAGTTGGAGTGCAATGGCGCGATCTTGGCTCACTGCAACCTCCGCCTCCGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCAAGTAGCTGTGATTCAGGCACGTGCCACCACACCAGCTAATTTTTGTATTTAATAGAAAACAGGGTTTACCCTGTTAGCCAGGCTGGTCTCAAACCTGACCTCAGATGATCCGCCCCGCTTGGCCCTCCCAAAGTGCTGGGATTACAGATGTGAGCCACCAGCCGCGCCGAGAGCACTTTTTTTTAAATGGCCTTGCACTCTTCTTATGGACCTTTGCTGCCCTCAGTTGACCAAACATGACATCAGAAACAGATACATTTGTGTGTTTTAAAAACAGCTCTCAATACTGG**

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