

Global gene expression analysis of *Escherichia coli* K-12 DH5 α after exposure to 2.4 GHz wireless fidelity radiation. Ilham H. Said-Salman, Fatima A. Jebaii, Hoda H. Yusef, Mohamed E. Moustafa.

Table S1. Up-regulated genes after exposure to 2.4 GHz Wi-Fi for 5 hours. A single gene may be implicated in more than one GO process.

Gene names	Putative function	GO term
<i>cheR</i>	Chemotaxis, protein methylation	Chemotaxis (GO:0006935) Metabolic process (GO:0008152)
<i>cheY</i>	Chemotaxis, protein acetylation Signal transduction system	Bacterial-type flagellum-dependent cell motility (GO:0071973) Chemotaxis (GO:0006935) Biological regulation (GO:0065007) Metabolic process (GO:0008152)
<i>motB</i>	Motility protein B, chemotaxis	Bacterial-type flagellum-dependent cell motility (GO:0071973) and chemotaxis (GO:0006935)
<i>fliC</i>	Flagellin	Bacterial-type flagellum-dependent cell motility (GO:0071973)
<i>fliT</i>	Flagellar protein, negative regulation of bacterial-type flagellum assembly, flagellum organization, protein folding	Bacterial-type flagellum-dependent cell motility (GO:0071973) Biological regulation (GO:0065007)
<i>fliL</i>	Flagellar protein, chemotaxis	bacterial-type flagellum-dependent swarming motility (GO:0071973) Chemotaxis (GO:0006935)
<i>fliM</i>	Flagellar motor switch protein, chemotaxis	Bacterial-type flagellum-dependent cell motility (GO:0071973) Chemotaxis (GO:0006935)
<i>flgG</i>	Flagellar basal-body rod protein	Bacterial-type flagellum-dependent cell motility (GO:0071973)
<i>fimI</i>	Fimbrin-like protein, pilus organization	Cell adhesion and biofilm (GO:0043709)
<i>pgaD</i>	Biofilm PGA synthesis protein	Cell adhesion and biofilm (GO:0043709)
<i>yadC</i>	Fimbrial-like protein, response to DNA damage, pilus organization, response to antibiotic	Cell adhesion and biofilm (GO:0043709) Response to stimulus (GO:0050896)
<i>yadM</i>	Fimbrial-like protein, pilus organization	Cell adhesion and biofilm (GO:0043709)
<i>insH21</i>	Transposase activity, Involved in the transposition of the insertion sequence IS5.	Transposition, DNA-mediated (GO:0006313), Metabolic process (GO:0008152)
<i>insH1</i>	Transposase activity, Involved in the transposition of the insertion sequence IS5.	Transposition, DNA-mediated (GO:0006313), Metabolic process (GO:0008152)

<i>insH2</i>	Transposase activity, Involved in the transposition of the insertion sequence IS5.	Transposition, DNA-mediated (GO:0006313), Metabolic process (GO:0008152)
<i>insH3</i>	Transposase activity, Involved in the transposition of the insertion sequence IS5.	Transposition, DNA-mediated (GO:0006313), Metabolic process (GO:0008152)
<i>insH4</i>	Transposase activity, Involved in the transposition of the insertion sequence IS5.	Transposition, DNA-mediated (GO:0006313), Metabolic process (GO:0008152)
<i>insH7</i>	Transposase activity, Involved in the transposition of the insertion sequence IS5.	Transposition, DNA-mediated (GO:0006313), Metabolic process (GO:0008152)
<i>insH8</i>	Transposase activity, Involved in the transposition of the insertion sequence IS5.	Transposition, DNA-mediated (GO:0006313), Metabolic process (GO:0008152)
<i>insH9</i>	Transposase activity, Involved in the transposition of the insertion sequence IS5.	Transposition, DNA-mediated (GO:0006313), Metabolic process (GO:0008152)
<i>insH10</i>	Transposase activity, Involved in the transposition of the insertion sequence IS5.	Transposition, DNA-mediated (GO:0006313), Metabolic process (GO:0008152)
<i>insH11</i>	Transposase activity, Involved in the transposition of the insertion sequence IS5.	Transposition, DNA-mediated (GO:0006313), Metabolic process (GO:0008152)
<i>insH12</i>	Transposase activity, Involved in the transposition of the insertion sequence IS5.	Transposition, DNA-mediated (GO:0006313), Metabolic process (GO:0008152)
<i>oxc</i>	Response to acidic pH, oxalate catabolic activity	Response to stimulus (GO:0050896), Metabolic process (GO:0008152)
<i>yjjQ</i>	Response to methylglyoxal, Regulation of transcription in response to methylglyoxal	Response to stimulus (GO:0050896) Biological regulation (GO:0065007)
<i>arsC</i>	Response to DNA damage stimulus; response to arsenic, Arsenate reductase activity	Response to stimulus (GO:0050896) Metabolic process (GO:0008152)
<i>sulA</i>	Cellular response to DNA damage stimulus; SOS response, Negative regulation of cell division	Response to stimulus (GO:0050896) Biological regulation (GO:0065007)
<i>sbcB</i>	DNA repair, Putative phosphotransferase enzyme IIB component	Response to stimulus (GO:0050896) Transport (GO:0006810)
<i>recT</i>	DNA renaturation, DNA synthesis Involved in double-strand break repair via homologous recombination	Response to stimulus (GO:0050896) Metabolic process (GO:0008152)
<i>ybhG</i>	Response to antibiotic	Response to stimulus (GO:0050896)
<i>ampE</i>	Response to antibiotic	Response to stimulus (GO:0050896)

<i>fliA</i>	Sigma factor responsible for initiation of transcription of genes involved in motility and flagellar synthesis	Biological regulation (GO:0065007)
<i>flgM</i>	Anti-sigma factor FlIA , negatively regulates flagellar genes	Biological regulation (GO:0065007)
<i>puuC</i>	Putrescine catabolic process	Metabolic process (GO:0008152)
<i>eutP</i>	Ethanolamine catabolic process	Metabolic process (GO:0008152)
<i>metC</i>	Methionine biosynthetic process	Metabolic process (GO:0008152)
<i>kbaY</i>	Carbohydrate metabolic process	Metabolic process (GO:0008152)
<i>sgcB</i>	Kinase activity	Metabolic process (GO:0008152)
<i>malP</i>	Glycogen catabolic process	Metabolic process (GO:0008152)
<i>malZ</i>	Oligosaccharide catabolic process	Metabolic process (GO:0008152)
<i>rhmR</i>	Transcription factor activity	Biological regulation (GO:0065007)
<i>alpA</i>	Biofilm formation Prophage CP4-57 regulatory protein	Biological regulation (GO:0065007)
<i>ykfJ</i>	Pseudogene	RNA processing (GO:0006396)
<i>agaR</i>	Repressor for the aga operon for N-acetyl galactosamine transport and metabolism.	Biological regulation (GO:0065007)
<i>yhdX</i>	Putative amino-acid ABC transporter permease protein	Transport (GO:0006810)
<i>agaC</i>	N-acetylgalactosamine permease IIC component 1	Transport (GO:0006810)
<i>yehC</i>	Chaperone-mediated protein folding	Cell wall organization (GO:0071555)
<i>yehR</i>	Lipid-anchor	Plasma membrane (GO 0005886)
<i>nlpA</i>	Lipid-anchor, plasma membrane methionine transport	Plasma membrane (GO 0005886)
<i>essQ</i>	Prophage lysis protein	cytolysis (GO:0019835)

Table S2. Down-regulated genes after exposure to 2.4 GHz Wi-Fi for 5 hours. A single gene may be implicated in more than one GO process.

Gene names	Putative function	GO term
<i>alsC</i>	Carbohydrate transport	Localization and transport (GO:0051179)
<i>gadC</i>	Amino acid transport, maintain a near-neutral intracellular pH	Localization and transport (GO:0051179) Biological regulation(GO:0065007)
<i>ompL</i>	Oligosaccharide and ion transport	Localization and transport (GO:0051179)
<i>ppdB</i>	Protein secretion by the type II secretion system	Localization and transport (GO:0051179)
<i>ssuA</i>	Alkanesulfonate transport, Sulfur compound metabolic process	Localization and transport (GO:0051179) Metabolic process (GO:0008152)
<i>xanP</i>	Xanthine transport	Localization and transport (GO:0051179)

<i>ycaD</i>	transmembrane transport	Localization and transport (GO:0051179)
<i>ytfT</i>	transmembrane transport	Localization and transport (GO:0051179)
<i>insL1</i>	Involved in the transposition of the insertion sequence IS186.	Transposition, DNA-mediated process (GO:0006313) Metabolic process (GO:0008152)
<i>insL2</i>	Involved in the transposition of the insertion sequence IS186.	Transposition, DNA-mediated process (GO:0006313) Metabolic process (GO:0008152)
<i>insL3</i>	Involved in the transposition of the insertion sequence IS186.	Transposition, DNA-mediated process (GO:0006313) Metabolic process (GO:0008152)
<i>pyrI</i>	Pyrimidine nucleotide biosynthetic process	Metabolic process (GO:0008152)
<i>purE</i>	'De novo' IMP biosynthetic process	Metabolic process (GO:0008152)
<i>rimO</i>	Peptidyl-L-beta-methylthioaspartic acid biosynthetic process from peptidyl-aspartic acid; tRNA modification	Metabolic process (GO:0008152)
<i>cobC</i>	Cobalamin biosynthetic process	Metabolic process (GO:0008152)
<i>fdnI</i>	Anaerobic respiration; formate oxidation; respiratory electron transport chain	Metabolic process (GO:0008152)
<i>fdnH</i>	Anaerobic respiration; formate oxidation; respiratory electron transport chain	Metabolic process (GO:0008152)
<i>fdnG</i>	Anaerobic respiration; formate oxidation; respiratory electron transport chain	Metabolic process (GO:0008152)
<i>alsK</i>	D-allose catabolic process	Metabolic process (GO:0008152)
<i>appB</i>	Aerobic electron transport chain; oxidative phosphorylation	Metabolic process (GO:0008152)
<i>hyi</i>	Glyoxylate metabolic process	Metabolic process (GO:0008152)
<i>eutQ</i>	Ethanolamine catabolic process	Metabolic process (GO:0008152)
<i>hyaB</i>	Anaerobic respiration; fermentation	Metabolic process (GO:0008152)
<i>hyaA</i>	Anaerobic respiration; fermentation	Metabolic process (GO:0008152)
<i>hyaD</i>	Protein processing	Metabolic process (GO:0008152)
<i>pyrB</i>	'De novo' pyrimidine nucleobase biosynthetic process; cellular amino acid metabolic process; nitrogen compound metabolic process	Metabolic process (GO:0008152)
<i>purN</i>	'De novo' IMP biosynthetic process, cellular response to DNA damage stimulus	Metabolic process (GO:0008152) Response to stimulus (GO:0050896)
<i>udp</i>	Uridine catabolic process, cellular response to DNA damage stimulus	Metabolic process (GO:0008152) Response to stimulus (GO:0050896)
<i>lpp</i>	Lipid modification	Metabolic process (GO:0008152)
<i>yafO</i>	SOS response, Negative regulation of translation, DNA repair	Response to stimulus (GO:0050896) Biological regulation (GO:0065007)

		Metabolic process (GO:0008152)
<i>yjiE</i>	Regulation of transcription, DNA-templated	Biological regulation(GO:0065007)
<i>yadV</i>	Probable fimbrial chaperone	Cell adhesion (GO:0071555)
<i>yciG</i>	Flagellum-dependent swarming motility	Bacterial-type flagellum-dependent swarming motility (GO:0071978)
<i>yidG</i>	Inner membrane protein	integral component of membrane (GO:0016021)
<i>yddB</i>	Pseudogene	integral component of membrane (GO:0016021)
<i>appX</i>	Part of cytochrome bd-II oxidase	Plasma membrane (GO:0005886)
<i>zapA</i>	Activator of cell division	Cell division (GO:0000917)
<i>ldrA</i>	Toxic component	Plasma membrane (GO:0005886)
<i>ldrB</i>	Toxic component	Plasma membrane (GO:0005886)
<i>ldrC</i>	Toxic component	Plasma membrane (GO:0005886)
<i>yqhh</i>	Peptidoglycan binding, cell outer membrane	intrinsic component of cell outer membrane (GO:0031230)

Table S3. QRT-PCR primer sets used in this study and their target genes.

Gene name	Forward primer	Reverse primer	Amplicon size
<i>pgaD</i>	TTACGACCCGACAATCACCCAG	GCCAGTAATAACCCGTCAGCA	123
<i>fliC</i>	ATTCCGTTCTTCCTCGGTG	TGGACACTTCGGTCGCATAG	131
<i>cheY</i>	AGTGCGTAACTGCTGAAAGA	AAATCCATAACCGCCTGCCT	100
<i>malP</i>	TCGGCTATCGTAATGGCGTG	TTCGGCACGCAAGAAATCAC	107
<i>malZ</i>	CAGGTGCTGTATGCCGAAGA	CACGGCATTGAGAAACGGTG	132
<i>motB</i>	GAATGATGGTCGGAGGGTT	GCCTGTTCGGCTTGTGTTTC	146
<i>alsC</i>	AACTGATGTTGGCAGGTGTTG	AGGGTGATGATGAACGGGTG	130
<i>alsK</i>	CGATCTTTTCGTCATGCGG	GAAGGCGGGCATATCCATCA	142
<i>appB</i>	CGACGGATTGACATGGGGA	AAATAATGCCCCACCAAGCGA	142
<i>appX</i>	GTATTTACTTTGGTTCGTCGGCA	GGTCCAGCCATACCAACACA	71
<i>gyrA*</i>	GTCGTGGCGGAAAGGTAAA	CGGCTGGAGAAGCACAGAA	106
<i>frr*</i>	GATCTTGGCCTGAACCCGAA	CTGCTTCACCACGAACGATTT	109

*housekeeping genes