Ni is recognized as an element that is toxic to humans, acting as an allergen and a carcinogenic agent, and it is also toxic to plants. The toxicity of Ni has been understudied in microorganisms. The data presented here were obtained by submitting the model bacterium Escherichia coli K-12 to nickel stress. To identify expressed genes, RNA-Seq was performed. Bacteria were exposed to 50 μM NiCl₂ during 10 min. Exposure to Ni lead to the deregulation of 57% of the E. coli transcripts. Further analysis using DAVID identified most affected biological pathways. The list of differentially expressed genes and physiological consequences of Ni stress are described in "Ni exposure impacts the pool of free Fe and modifies DNA supercoiling via metal-induced oxidative stress in Escherichia coli K-12" (M. Gault, G. Effantin, A. Rodrigue, 2016) [1].

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How data was acquired
High-throughput RNA-sequencing

Data format
Filtered and analyzed with statistical tests

Experimental factors
The bacteria were grown in minimal medium until early log-phase where 50 μM NiCl₂ was added, after 10 min bacteria were harvested and frozen

Experimental features
Total RNA was extracted using the frozen acid-phenol method. ARNr were excluded. Directional libraries were sequenced on Illumina Hiseq2500 in single reads.

Data source location
Laboratory “Microbiologie, Adaptation et Pathogénie”, UMR5240, INSA Lyon, France

Data accessibility
Data are with this article and deposited in NCBI’s Gene Expression Omnibus (GEO), accessible through GEO Series accession number GEO: GSE76167 http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE76167

Value of the data

- Ni, as many transition metals, is essential as a trace element to living organisms whereas it becomes toxic when present in excess. At present, the description of Ni toxicity in bacteria is under-studied although this metal is a widespread element bacteria are in contact with.
- The data shows differentially expressed genes under Ni stress that could be compared to differentially expressed genes in other metal-stress conditions or other stress conditions.
- Analysis of the biological pathways impacted when cells are exposed to Ni will help to understand the molecular mechanisms of Ni- or metal-stress.
- Identification of Ni-deregulated genes could lead to biotechnological applications such as the design of whole cell biosensors.

1. Data

The RNA-Seq and gene expression datasets were deposited in NCBI’s Gene expression Omnibus [2], accessible through GEO series accession number GEO: GSE76176. Fig. 1 shows the distribution of deregulated genes in E. coli upon exposure to 50 μM Ni. 2545 genes were deregulated considering a Fold-Change (FC) of 1.5, representing 57 % of the 4440 annotated transcripts of E. coli K-12 strain W3110. Gene Ontology was applied to classify differentially expressed genes according to their biological function (see Fig. 1 in [1]). GO Terms that were enriched in the list of differentially expressed genes were identified using the DAVID tools (Database for Annotation, Visualization and Integrated Discovery) [3,4]. Pathways that were significantly affected were mapped using KEGG and are listed in Table 1.

2. Experimental design, materials and methods

2.1. Strains and growth conditions

E. coli K-12 cells were grown at 37 °C in minimal medium supplemented with glucose until O. D₆₀₀nm = 0.3 and then treated with 50 μM NiCl₂ during 10 min. These conditions lead to maximal expression of the Ni-stress marker gene rcnA (see Fig. S1A and S1B in [1]).
2.2. RNA extraction and RNA-Seq

Three samples of each condition were treated, as described in [1].

2.3. Data analysis

Strand-orientated RNA-Seq was performed on Illumina Hiseq2500. Basecalls were performed using HCS 2.0.5 and RTA 1.17.20. Reads were aligned to whole reference genome *Escherichia coli* K-12 W3110 NC_007779 using CASAVA v 1.8.2 software (Illumina). Gene expression was determined using Cufflinks v. 2.0.2. software. Differentially expressed genes were identified as described in [1].
2.4. Identification of the affected pathways from the differentially expressed genes

Online tool DAVID (http://david.abcc.ncifcrf.gov/) [3,4] was used to find out the affected pathways among the differentially expressed gene lists. The gene lists were uploaded with selecting the background as all the genes of *E. coli*. Functional Annotation Chart was visualized using the p-value threshold of 0.01 and a minimum number of genes of 4. The information regarding the affected pathways was obtained from Kyoto Encyclopedia of Genes and Genomes (KEGG) within the analysis in DAVID, using the mentioned thresholds.

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Transparency document. Supplementary material

Transparency data associated with this article can be found in the online version at http://dx.doi.org/10.1016/j.dib.2016.08.069.

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