ERRATUM

In the article "Gene regulatory network inference and analysis of multidrug-resistant *Pseudomonas aeruginosa*", DOI number: 10.1590/0074-02760190105, published in *Mem Inst Oswaldo Cruz*, Rio de Janeiro, Vol. *114*: e190105, 2019:

On page 7, Table I, where it reads:

"PA4851 19380"

It should read:

"AL347 05155"

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"Table II shows a comparison of network statistics between the CCBH4851 GRN and the GRN network published by Galán-Vásquez et al. (12) One clear trend is that the CCBH4851 GRN represents a substantial improvement in terms of network completeness, since is includes more nodes, edges and network motifs."

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On page 4, Fig. 2 should be replaced by the figure below:

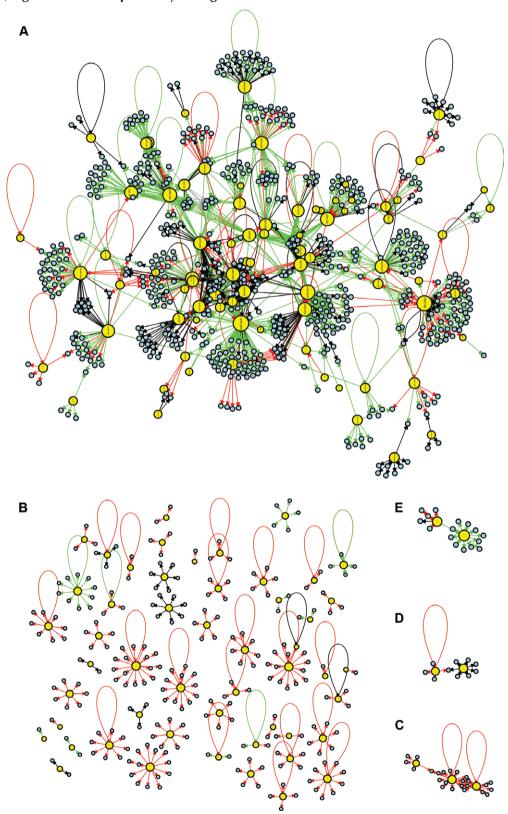


Fig. 2: visualisation of the *Pseudomonas aeruginosa* CCBH4851 gene regulatory network (GRN). Yellow circles indicate regulatory genes, light blue circles indicate target genes (TGs), black lines indicate an unknown mode of regulation, green lines indicate activation, red lines indicate repression and grey lines indicate a dual mode of regulation. A: the GRN large highly connected network component; B: all regulatory and TGs that have no connections with the component depicted in A; C-E: clusters of lower connectivity compared to the component depicted in A. All figures are presented with higher resolution in the Supplementary data.

On page 8, Fig. 4 should be replaced by the figure below:

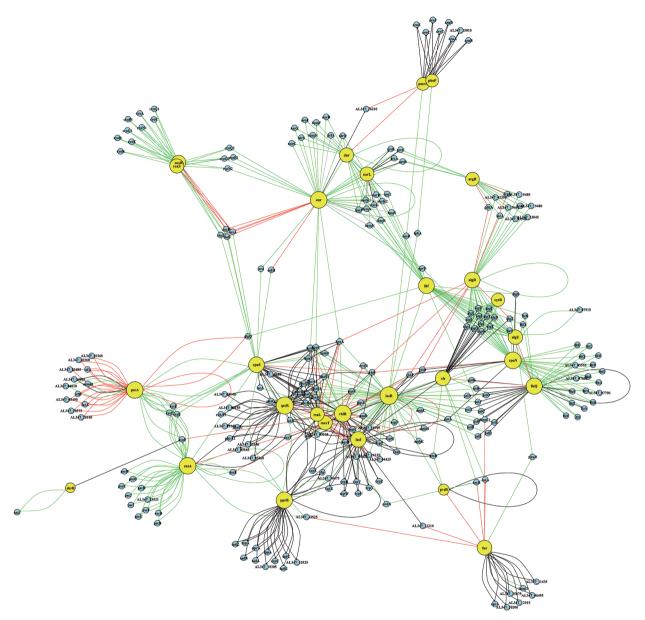


Fig. 4: connectivity relationships among the 30 most influential hubs of the *Pseudomonas aeruginosa* CCBH4851 gene regulatory network. Yellow circles indicate regulatory genes considered hubs, light blue circles indicate target genes, black lines indicate an unknown mode of regulation, green lines indicate activation, red lines indicate repression and grey lines indicate a dual mode of regulation.

The Supplementary material were corrected and attached in the link below:

https://memorias.ioc.fiocruz.br/images/revistas/2020/115/0105er_sd.xlsx