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Correction to: Identification of two different chemosensory pathways in representatives of the genus *Halomonas*

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Correction

Following the publication of this article [1], the authors noticed that Fig. 3 was missing. In that figure, one of the numbers corresponding to the *Halomonas* chemoreceptors was missing: namely, chemoreceptor 07070. The correct version of Fig. 3 has been included in this Correction.

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Reference
1. Gasperotti AF, et al. BMC Genomics. 2018;19:266.

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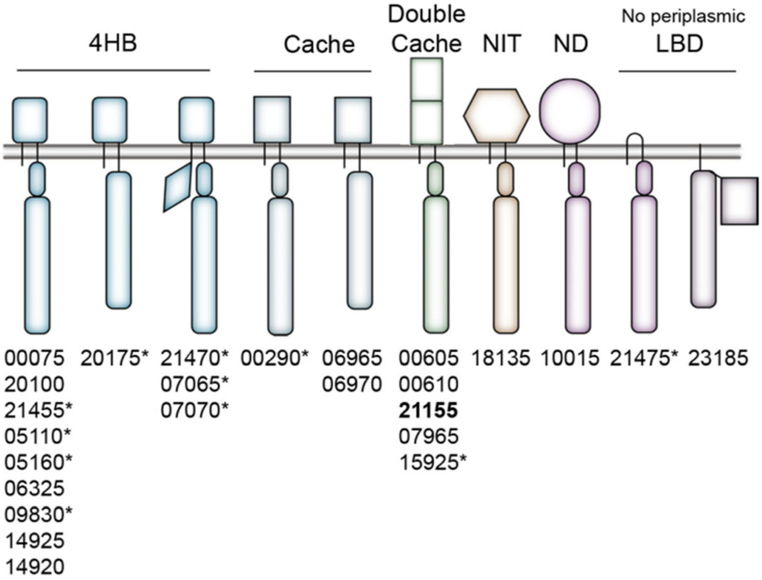

Fig. 3 Schematic representation of chemoreceptors encoded in the genome of H. titanicae KHS3. MCPs are grouped according to the predicted structure of the periplasmic LBD: 4-helix bundle (4HB, rectangle with curved edges), Cache (rectangle), double Cache (double rectangle), nitrate-nitrite sensing fold (NIT, hexagon), not determined (ND, circle) and those with no periplasmic LBD. The gray horizontal bar represents the cytoplasmic membrane. MCP cytoplasmic subdomains are represented by a long rectangle (conserved cytoplasmic domain or signaling domain), an oval representing the HAMP domain, a diamond shape representing PAS domain. The rectangle at the C-terminus of RO22_23185 represents a Cache domain. The corresponding MCP ID numbers are listed below each kind of MCP (all ID numbers should be preceded by "RO22_" following the IMG gene annotation). Asterisks indicate the presence of C-terminal pentapeptide for interaction with CheR. All MCPs belong to the 36H family except one, which belongs to the 40H family (shown in bold)