



CORRECTION

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Correction: Comparing the genomes of *Helicobacter pylori* clinical strain UM032 and mice-adapted derivatives

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Correction

After publication of this work [1], we discovered that due to an inadvertent mistake, Figures 4 and 5 in the original

article were essentially the same figure. Amendment to Figure 5 (Figure 1 here) has now been added. We offer our sincerest apologies for this oversight.

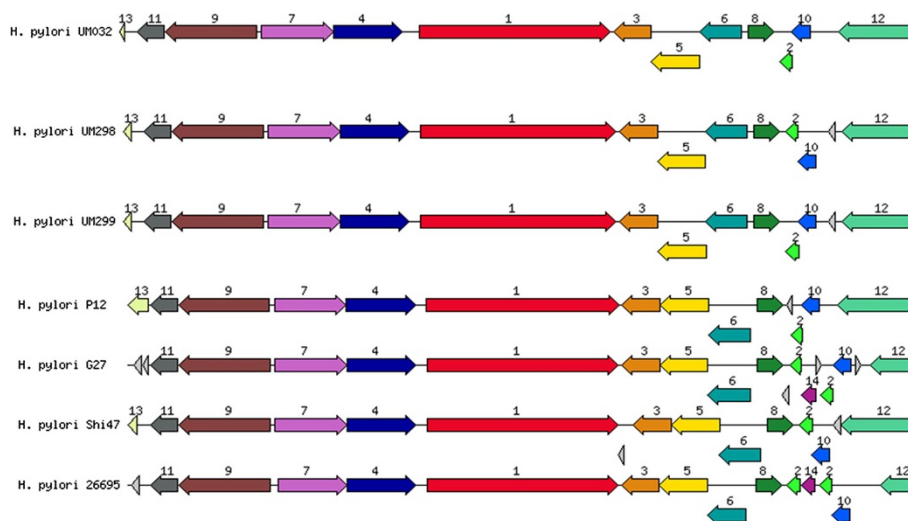


Figure 1 Genetic relatedness of *vacA* cluster with closely related bacteria. 1: vacuolating cytotoxin, 2: hypothetical protein, 3: haemin uptake system ATP-binding protein, 4: cysteinyl-Trna-SYNTHEase, 5: IRON III, 6: dehydrogenases with different specificities, 7: proposed peptidoglycan lipid, 8: hypothetical protein, 9: hypothetical protein, 10: DNA damage inducible protein J, 11: holliday junction DNA helicase RUUA, 12: putative outer membrane protein, 13: hypothetical protein.

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1. Khosravi Y, Rehvathy V, Wee WY, Wang S, Baybayan P, Singh S, Ashby M, Ong J, Amoyo AA, Wee SS, Choo SW, Perkins T, Chua EG, Tay A, Marshall BJ, Loke MF, Goh KL, Pettersson S, Vadivelu J: **Comparing the genomes of *Helicobacter pylori* clinical strain UM032 and Mice-adapted derivatives.** *Gut Pathog* 2013, **5**:25.

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