Erratum to the "Report on the second annual in vitro external quality assessment scheme for WGS-based resistome profiling of *Salmonella* and *Campylobacter*" from 2023.

Missing information was discovered in Table 13 thanks to the feedback from one of the participants. The authors of the report apologize for the misunderstanding. Corrections to the table and the text should be introduced as follows:

Presence of the point mutation 23S A2075G should have been marked for the provider's reference dataset, AMR_Ref. The mutation was detected by the provider using AMRFinderPlus, however, not shown in this table due to human error.

The correct table should be:

"Table 1. Point mutations (PMs) reported in Campylobacter strain EQA2-C23-01. Reference datasets, Res_Ref and AMR_Ref, are shaded grey. Participants are grouped based on database(s) used: Green – PointFinder, Blue – AMRFinderPlus with or without PointFinder. Percentage concordance is based on following scale: darkest orange colour: 100% concordance among participants, lighter orange colour: 90-99% concordance, lightest orange colour: 80-89% concordance. Concordance lower than 80% is without colour.

	PointFinder													AMRFinderPlus +/- PointFinder											0			
	Res_Ref	E28	B1	E08	B3	E13	B35	E09	E05	E03	E16	E07	E20	E29	E32	AMR_Ref	E21	E24	E27	E10	E02	E36	E23	E22	E14	E19	E12	dance
PointFinder								*																				0.0
AMRFinderPlus																												lo ₂
Other database																											**	%
23S A2075G	Χ	Χ	Χ	Х	Х	Х	Х	Х	Х	Х	Х	Х	Χ	Х	Х	Χ			Х	Χ	Х	Χ	Х	Х	Х	Х	Х	92
gyrA T86I										Х			Х			Х	Х	Х		Х	Х	Χ	Х		Х		Х	
gyrA_2 T86I	Х	Х	Х	Х	Х	Х	Х	Х	Х			Х		Х					Х					Х		Х		92
50S L22 A103V																Х	Х	Х	Х	Χ		Χ	Х	Х	Х			32

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Subsequently, mentioning of this mutation in the AMR_Ref in the text should be corrected in the following way:

"In point mutations reporting ("Table 1), differences between reference datasets were observed. The mutation 50S L22 A103V was reported in AMR_Ref dataset, but not in Res_Ref. This difference is related to the fact that the mutation in 50S is only present in the AMRFinderPlus database. The gyrA T86I substitution was reported in both datasets but either as gyrA_2 (Res_Ref) or gyrA (AMRFinderPlus)."

^{**} ResFinder, Card, NCBI, home-made database"