CORRIGENDUM

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Corrigendum: A CRISPR/Cas system mediates bacterial innate immune evasion and virulence

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In this Letter, we described two small RNAs (scaRNA and tracrRNA) within the *Francisella novicida* CRISPR/Cas locus that are necessary for repression of an endogenous transcript. Concurrent to our studies, E. Charpentier's group performed RNA sequencing analyses of multiple type II CRISPR loci to identify tracrRNA in *F. novicida* and other species[1], based in part on the co-processing of tracrRNA:crRNA by RNase III (ref. 2). These observations indicate that the regulatory RNA we annotated as scaRNA is the tracrRNA, and that the RNA we annotated as tracrRNA is the scaRNA. Furthermore, RNAseq data show that the transcriptional direction of the crRNA array is the opposite of what was predicted. Finally, our predictions of tracrRNA and scaRNA within Supplementary Table 2 are incorrect based on this transcriptional analysis; the scaRNAs predicted in *Neisseria meningitidis* 92045, *Listeria monocytogenes* SLCC2482 and *Streptococcus pyogenes* M1 GAS are in fact within the crRNA array transcript, as is the predicted tracrRNA in *Campylobacter jejuni* NCTC11168, whereas the predicted *C. jejuni* scaRNA is actually the tracrRNA. We include a corrected annotated Fig. 1a below, and apologize for any confusion about our incorrect nomenclature. We are grateful to E. Charpentier and her group for alerting us to the errors.

1. Chylinski, K., Le Rhun, A. & Charpentier, E. The tracrRNA and Cas9 families of type II CRISPR-Cas immunity systems. *RNA Biol.* **10,** 726–737 (2013).
2. Deltcheva, E. *et al.* CRISPR RNA maturation by *trans*-encoded small RNA and host factor RNase III. *Nature* **471,** 602–607 (2011).

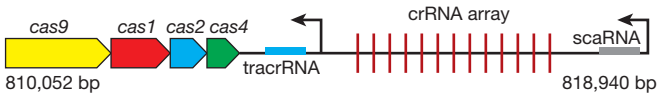

Figure 1 | This is the corrected Fig. 1a of the original Letter.

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