Variation in the *Neisseria meningitidis* FadL-like protein: an evolutionary model for a relatively low-abundance surface antigen

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The shading patterns in Fig. 2(a) of the published version of this paper (page 3601) were not correctly reproduced. The correct version of the figure is shown below.

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**Fig. 2.** (a) Diagram illustrating the variability of VR1 and VR2 coding regions in fadL sequences from the four variants, subvariant 1a and the four commensals. Fragments with sequence identity higher than 85% are indicated with the same pattern. The potential breakpoint for recombination (position 765) is indicated by a vertical line. The positions of two sites with high evidence of positive selection are indicated by circles. (b, c) Neighbour-joining trees constructed from the aligned nucleotide sequences encoding loops 3 (VR1) (b) and 4 (VR2) (c) of the FadL protein.