



Fig. 3. Normalised histograms h of the number of coverage n (*a*, *c*) and the residuals between the total and maximum numbers of coverages m (*b*, *d*) for non-SNP (*a*, *b*) and SNP (*c*, *d*) sites.

Approximations are made by the density functions of the beta n_b (black) and normal n_g (red) distributions; parameter estimates are $\alpha = 1.57$ (standard error is equal 0.02), $\beta = 7.9$ (0.2), and $\mu = 9.2$ (1.1), $\sigma = 25.9$ (0.7) for the fragment *a*; $\alpha = 0.5$ (standard error is equal 0.05), $\beta = 20$ (2) for the fragment *b*; $\alpha = 1.45$ (standard error is equal 0.02), $\beta = 8.4$ (0.2), and $\mu = 5.8$ (1.6), $\sigma = 25.2$ (0.8) for the fragment *c*; $\alpha = 1.71$ (standard error is equal 0.05), $\beta = 7.7$ (0.3), and $\mu = 5.3$ (0.6), $\sigma = 9.2$ (0.6) for the fragment *d*