SUPPLEMENTARY FIGURES



FIG. S1: Panels on the first line: same as Fig. 2 (without the OU analysis) but considering bins of length $\ell = 500$ bp instead of $\ell = 1000$ bp to compute GC contents, showing that characteristic lengths are similar with shorter bins. Panels on the second line: same as Fig. 2 (without the OU analysis) but considering the 861 genomes of length ≥ 500 kb from the STRING database that we discarded in the main figures because of their unsuitability for the evolutionary analysis (see Methods).



FIG. S2: Characteristic lengths d_{GC1} , d_{GC2} and d_{GC3} computed respectively from the first, second and third base of codons, as a function of the characteristic length d_{GC} of the overall GC signal, showing that the highest correlation is obtained with the third base.



FIG. S3: Characteristic lengths from evolutionary conservation of gene context. As in Fig. 4, but showing here how the characteristic lengths d_{synt} vary as a function of f_{\min} , the frequency above which two genes are considered in synteny, for a given genome (the genome of *E. coli* in red and of *B. subtilis* in green). The two plateaus around 15 kb and 30 kb, which are particularly stricking for *E. coli* (red), show that the two modes of Fig. 4B can also be observed within a given genome.