

Fig. S9

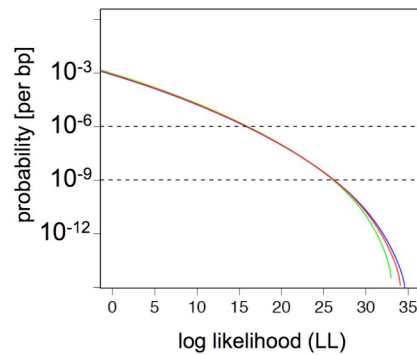


Figure S9. Background distribution for the likelihood (LL, cf. methods) score (in bits) of the E1-E2 model computed using the saddle point method as in [1]. The graph shows the per site probability to find a hit with score above the value in the x-axis. We considered single nucleotide background frequencies from the non-repetitive portions of the mouse (green), *D. Melanogaster* (blue) and *fugu* (red) genomes, which give very similar results. Agreement with empirical distributions is excellent.

Reference :

1. Djordjevic M, Sengupta AM, Shraiman BI (2003) A biophysical approach to transcription factor binding site discovery. *Genome Res* 13: 2381-2390.