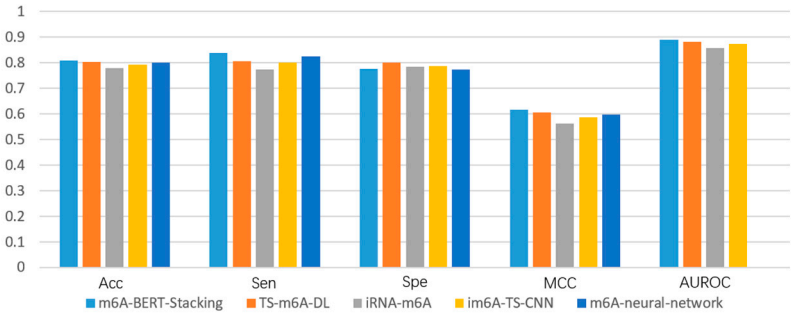
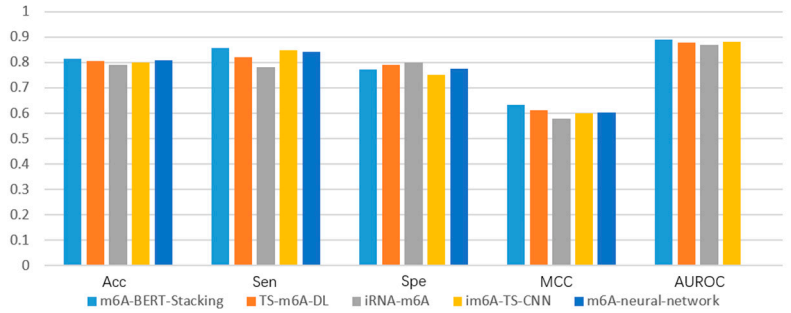


Figure S1. The nucleotide composition preferences between positive and negative samples on the remaining 10 datasets. (a) H_k benchmark dataset; (b) H_l benchmark dataset; (c) M_b benchmark dataset;

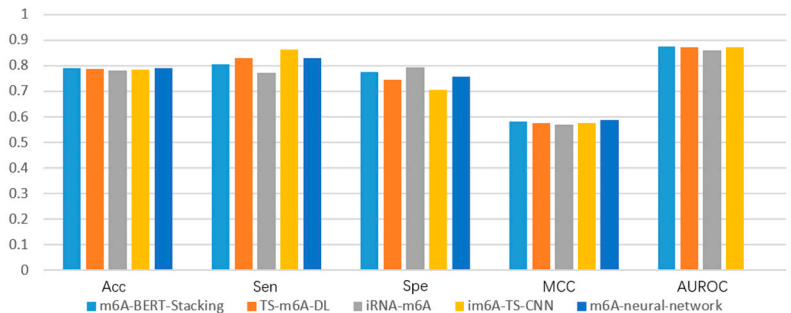
(d) M_h benchmark dataset; (e) M_k benchmark dataset; (f) M_l benchmark dataset; (g) M_t benchmark dataset; (h) R_b benchmark dataset; (i) R_k benchmark dataset; (j) R_l benchmark dataset.



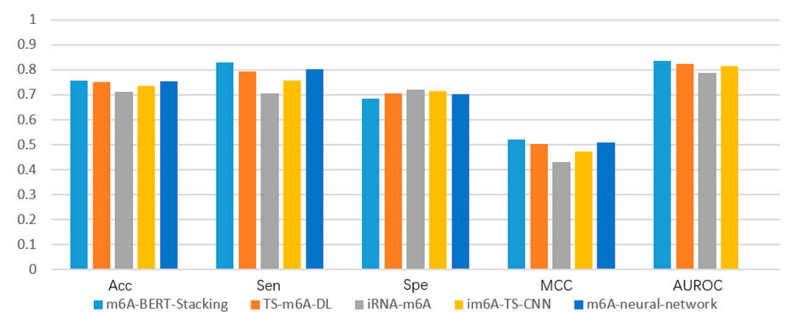
(a)



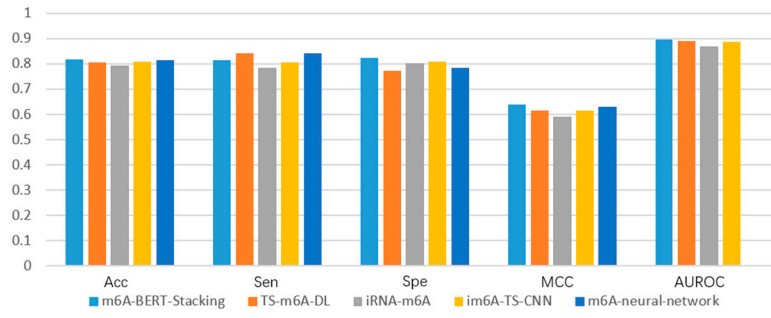
(b)



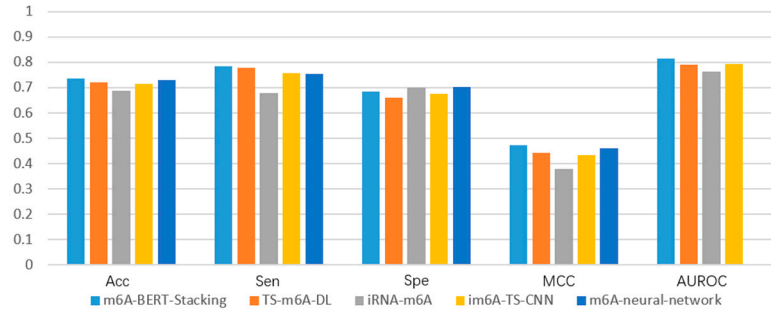
(c)



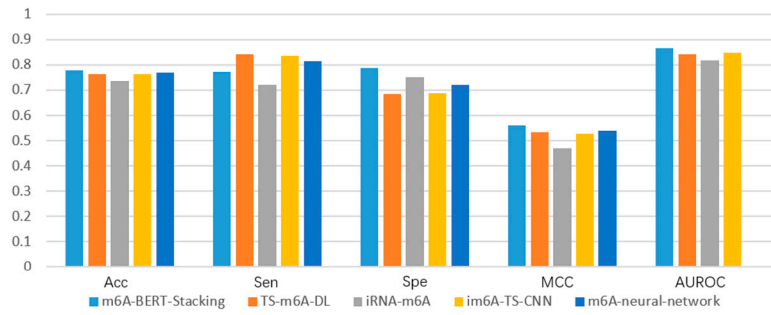
(d)



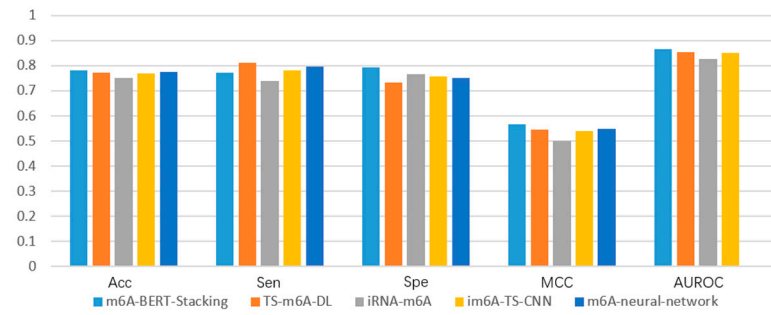
(e)



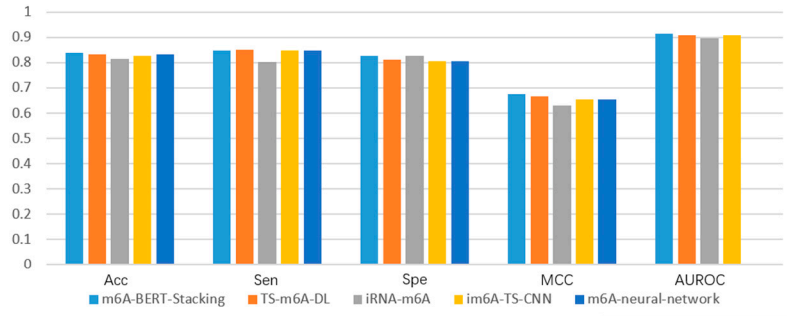
(f)



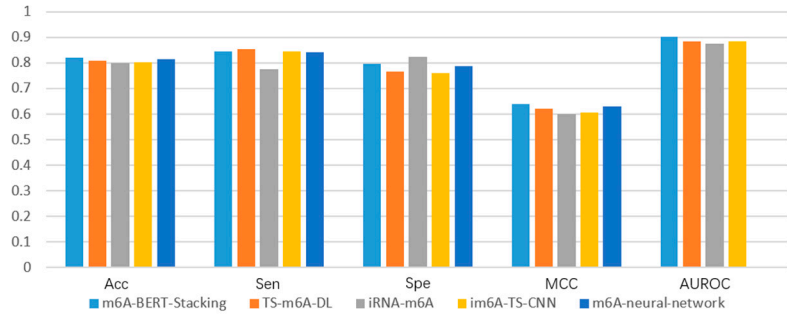
(g)



(h)



(i)



(j)

Figure S2. Performance comparison between different models on the remaining 10 datasets. (a) H_k independent dataset; (b) H_l independent dataset; (c) M_b independent dataset; (d) M_h independent dataset; (e) M_k independent dataset; (f) M_l independent dataset; (g) M_t independent dataset; (h) R_b independent dataset; (i) R_k independent dataset; (j) R_l independent dataset.